AL646080 Ralstonia AF127374 Streptomy A60304 Sequence 4 AR144763 Sequence AX097457 Sequence AE004755 Pseudomon

AL442629 Streptomy AE004675 Pseudomon AB070947 Streptomy AL049754 Streptomy

Saccharopol

M54983 Saccharopol X63601 S.griseus s I15434 Sequence 10 AF102510 Mycobacte

AL442120 Streptomy L37200 Streptomyce AR159871 Sequence

AB018074 Streptomy E59713 Process for

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Title:
Perfect score:
Sequence:
                     Result
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                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB seq length: 0
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1209
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Com
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                   Description
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ORGANISM
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Streptomyces coelicolor A3(2).

Streptomyces coelicolor A3(2)

Streptomyces coelicolor A3(2)

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Actinomyceftales; Streptomycineae; Streptomycetaceae; Streptomyces.

1 (bases 1 to 39524)

1 (bases 1 to 39524)

Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J.,

Kinashi,H. and Hopwood,D.A.

A set of ordered cosmids and a detailed genetic and physical map

for the 8 Mb Streptomyces coelicolor A3(2) chromosome

Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                      ABC transporter; adenylosuccinate synthetase; aspartate aminotransferase; ATP-dependent protease ATP-binding subunit; cytochrome P-450 hydroxylase; fba; fructose 1,6-bisphosphate aldolase; lipase/esterase; oxidoreductase; purA; RNA polymerase sigma factor; spermidine synthase; transmembrane efflux protein; two-component regulator; two-component sensor kinase; uridine
                                                                                                                                                                                                                                                                   AL049754.1 GI:4753846
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SHGCPIR
SC3F60
SC8F11
AF170880
SCF55
AF127374
AB048795
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STE250199
STE2505811
SFU08223
AB070940
SEERYABIO
AF322179
AE007165
MTV023
AF007022
STMSUBCB
AF079139
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AR159871
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AF127374
A60304
AR044763
AX097457
AE004755
AB018074
E59713
SCE41
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SERCP450A
AE004675
AB070947
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                                                                                                                                                                                                                                                                                                      39524 bp
cosmid H10.
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X60379 S.erythraea AF322179 Streptomy AE007165 Mycobacte AL022022 Mycobacte AF087022 Streptomy M32239 S.griseolus AF079139 Streptomy AF386507 Streptomy AF003014 Mesorhizo

AB070940 Streptomy X60379 S.erythraea U08223 Streptomyce AJ250199 Streptomy AJ250581 Streptomy

X86780 S.hygroscop AL445945 Streptomy AL353864 Streptomy AF170880 Streptomy AL132991 Streptomy AF127374 Streptomy

BCT 04-MAY-1999

AF072709 Streptomy AL450432 Streptomy AL391017 Streptomy AB070949 Streptomy AB070948 Streptomy

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FEATURES
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James, K.D., Parkill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
Submitted (05-MAY-1999) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 15A E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (URL: http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S.coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC.

Details of S. coelicolor sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97000351
2 (base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.nih.go.jp/
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                                                                                                                                                                                                                                                                                                                                                           >119 aa; probable CDS suggested by positional base preference, GC frame analysis and amino acid composition" (codon_start=1)
                                                                                                 DAYNSHSLALIEGLAGE"
                                                                                                                  /product-"hypothetical protein"
/protein_id-"CAB42010.1"
/protein_id-"CAB42010.1"
/db_xref-"G1:4753847"
/translation-"DPRIAAALAGVRRRGEEAQRAAAAGDLTVLIGYDLRYWRELATL
/translation-"DPRIAAALAGVRRRGEEAQRAAAAGDLTVLIGYDLRYWRELATL
/TRANSLCDFLHRLKYQSWVCTVQHLRRLSELRGALWSGHTALVDALARRDVPGARALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="A3(2)"
/db_xref="taxon:100226"
                               /gene="SCH10.01"
                                                                                                                                                                                                                                                                                                                                                                                                                             /note="SCH10.01, hypothetical protein, partial CDS, len:
>119 aa; probable CDS suggested by positional base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="SCH10.01"
                                                                                                                                                                                                                                                                                                /label=SCH10.01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="cosmid H10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Streptomyces coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note overlap with S.coelicolor cosmid
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overlap"
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sigE, Mycobacterium avium extracytoplasmic function alternative sigma factor (251 aa), fasta scores; opt: 226 z-score: 266.2 E(): 1.6e-07, 29.8% identity in 168 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="SCH10.03c"
/note="SCH10.03c, hypothetical protein, len: 96 aa;
/note="SCH10.03c, hypothetical protein, len: 96 aa;
unknown function, probable CDS suggested by positional
base preference, GC frame analysis and amino acid
composition"
complement(2749.
                                                                              /product="hypothetical protein"
/protein_id="CAB42014.1"
/db_xref="GI:4753851"
                                                                                                                                                                                                                                                                                                                                    complement(2472. .2672) /
/gene="SCH10.05c"
                                                                                                                                                                                                                                                                                                                                                                                           complement(2472. .2672)
/gene="SCH10.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tzanslation="MPARSDDMARQFELDRPRLRAVAYRILGSLGEADDALQEAMLRA
DRANTSEVGNESGWITTVVARVCINLLRARDTREEPLDDAARRQPAATGTAADPAEE
VOLADEVGIALLIVLDTLGPAERLAFVUHDMEDVPFDDIAAMLDKTPAATRGLASRA
RRVRGVPAPEADLPRRRRAVDAYLAATRGGDEDALVALLHPDVVLSADAAVVPTPEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1472. .2356)
/gene="SCH10.04c"
/note="SCH10.04c, probable RNA polymerase sigma
len: 294 aa; similar to many e.g. TR:005735 (EMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein"
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/db_xref==07:4753849"
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                       HLGPSLLLATGVLWPPGIVLVR
                                                                                                                                                                                                                                                   base preference and
                                                                                                                                                                                                                                                                             /note="SCH10.05c, hypothetical protein, i
unknown function, probable CDS suggested
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/transl_table=11
/label=SCH10.04c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1472. .2356)
/gene="SCH10.04c"
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/note="SCHIO.02, hypothetical protein, len: 221 aa;
unknown function, probable CDS suggested by positional
hase preference, GC frame analysis and amino acid
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                                                                                                                                                                  /label=SCH10.05c
                                                                                                                                                                                            /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MRSPLLACDLWLVPLVDVLCHTPDNPFAEELAQYDKVLAEAGLP
PVPVYQYMFOLSGEVAPVAGFDYDALHFLRRAHLLQVGGLPVTBVDELGGDYSOLLEM
FESTAQOSHLVWHYDHAGAYVPVDFPHPLSSSDELLAGGGPLGSSHTLLRELBAVAPAL
GIDPANPPAPPQPPLAPTELEEPAVPAPHDSSPFARERHVWLGLHAAATRSLAQGSMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1143.
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/protein_id="CAB42011.1"
/db_xref="GI:4753848"
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/label=SCH10.03c
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                                   GCCTGGCGGACGACCTGGTGGCCCGGCTGGTGGCGGCGGCGGCGGCGATCTGCTCACCG
                                                                                                                                                                                                                                                                                                            GCCTGGTGTCGAAGGCGTTCACGCCGCGCGCACCGTGGAGCCGCTGAAGCCGTACGTGCACG
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ACCGGGCCCCGCTGCCCCCTGGTCGGCGGAGATCTGCGGGATGTACGAGCTGAACCCGT 11078
                                                                                                                                                                                                                                                                                                                                                999t99teggcceggcgttctcgccgtccgcgctgccggctggaaccggtgatcgccg
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                                                                                                                                       gcaccgtggaccgcctgccgccctggcccgggggcgatggacgtggtcgacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adenylsucc_synt, Adenylosuccinate synthetase, score 742.40, E-value 1.9e-219, PS00513 Adenylosuccinate synthetase active site and PS01266 Adenylosuccinate
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/transl_table=11
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/note="corr
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/label=SCH10.06c
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Pred. No. 2.8e-12;
0; Mismatches 500;
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typhimurium dnaE gene;

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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAACCACGACCCGGCGGTCTTCACCGACCCGGAACGCCTCGACCTCACCCGCCGCGACA 10598
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                                                                                                                                             Andersen, J.F. and Hutchinson, C.R.
Andersen, J.F. and Hutchinson, C.R.
Characterization of Saccharopolyspora erythraea cytochrome P-450
genes and enzymes, including 6-deoxyerythronolide B hydroxylase
J. Bacteriol. 174, 725-735 (1992)
                                                                                                                                                                                                                                                                                                                                                                                   3078 bp DNA linear i Saccharopolyspora erythraea ORF 1 gene, partial cds; P-450 gene, complete cds; ORF 2 gene, partial cds M83]10
                                                                                                                                                                                                                                                               Saccharopolyspora erythraea
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae;
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                  /note="ORF homologous
                                         /tissue_lib="NRRL
<1. .859
                                                                        /organism="Saccharopolyspora
/db_xref="taxon:1836"
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to Escherichia putative"
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                    and
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SOURCE ORGANISM VERSION KEYWORDS RESULT 3 AE004675/c REFERENCE DEFINITION ACCESSION JOURNAL MEDLINE TITLE AUTHORS Stover.C.K., Pham,X.Q., Erwin,A.L., Mizoguchi,S.D., Warrene Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Le Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadman,S., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., I Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Paulsen,I.T. Complete genome sequence of Pseudomonas aeruginosa PAO1, ar opportunistic pathogen AE004675 Pseudomonas Nature 406 20437337 Pseudomonas Bacteria; Proteobacteria; Pseudomonas aeruginosa Pseudomonas ĀE004675 AE004091 AE004675.1 GI:9948522 (bases 1 to 10060) (6799), aeruginosa aeruginosa 10060 PA01, gamma subdivision; section DNA on 236 of linear BCT 529 of the Pseudomonadaceae; Larbig, K., Lim, R., Warrener, P., complete 30-AUG-2000 Lagrou, M., an

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Submitted (16-MAY-2000) Department of Medicine and Genetics,
Submitted (16-MAY-2000) Department of Medicine and Genetics,
University of Washington Genome Center, University Of Washington,
Box 352145, Seattle, WA 98195, USA
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Stover,C.K., Pham,X.-Q.T., Erwin,A.L., Mizoguchi,S.D., Warrener,P.,
Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J.,
Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E.,
Westbrook-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N.,
Folger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spencer,D.H.,
Wong,G.K.-S., Wu,Z., Paulsen,I.T., Reizer,J., Saier,M.H.,
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AINPGSNHWSFNPHYALTWSFFAEGWEASARLQYLLFGKNRDPAPPLADDYLQPGQAFH
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                                                                                                                                                                                                                                                                                                         complement(3008. .4342)
                                                                                                                                                                                                                                                         complement
                                                                                                                                                                                                                                                                                                                                            FLNAYHEYGARNRSEGSRLILRYSQVF"
                                                                                                                                                                                                                                                                                                                                                               {	t ANYSVSLALDAHWRLGLSGYSLRQITDERVDGHDRPDSRERVDAIGPALMFGWGKSRL}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="PA2473"
1429. .2073
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70. .1
                                                                                                                                                            transl_table=11/
                                                                                                                                                                                                                                                                                  /gene="PA2475"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="PA2473"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGRIGSIVGSLSGGALLGLGLGFSGILALLVIPALLAAVAVHRLGRRRARPSPTTL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GI:9948523"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                  (3008. .4342)
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7944.

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8621.

.9943

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SLGLGIGMPLLLLYTYGSRFLPKPGPMMNLYKGVFGFLFLGTAWILLRPLLGBALWIG
SLGLGIGMPLLLLYTYGSRFLPKPGPMMNLYKGVFGFLFLGTAWILLRPLLGBALWIG
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complement(6018. .7781)
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giiredseaksaallaskdpqkkalhdheqagkastlkplakipaavrkqlagnmelme
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RREPDLLRDFAEPLTIRVAAELFGFPREDTGQLLPWGRDLAAGLDLAASHGDAGQINR
SAVAFSDYLORQARGWSDGSSRPPSGAAPSILDGAAMLEAGLGLEDLVAAYAWVFMAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PALRRSLGVGASLGLAFWLLGSLGLGIYERGTRLPELSLRNAAGESVQLADFRGRPLV
INLWASWCPPCRREMPVLQQAQAENPDVVFLFANQGESAETVRHFLQGENLRLDNLLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(5182.
/gene="PA2477"
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/gene="PA2477"
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BASE COUNT
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Best Local S
Matches 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCGACAGCTTGCTGGAGCGCCGCGAGCCCGATCTGCTCAGGGATTTCGCCGAACCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gctgcggcccggccctggcccggggcgcgatggacgtggtcgacgagctggcgtacccgct
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                                                                                                                                                                                caccggccacgagacggtggccagccaggtgggcaacgccgtgctgagcctgctggcgca
                                                                                                                                                                                                                                           GATGCTGGAGGCCGGACTGGGCCTCGAGGACCTGGTAGCGGCCTATGCCATGGTGTTCAT
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                                                                                                                                                                                                                                                                                                                                                  ggcctcgcgaggcggcgtgagggcggcgaggacctgctggcgttgatgctcgacgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTGCTGCGCTTCGATGGCGCGGTGCGCGCGGCGTGCGTTGCACCCTGGAGGAGGTGGA
                                                                                                                                                             GGCCGCCTTCGAAACCACCATCAGCATGGTCGGCAACGCTACGCTGGCGCGCTGCTCACCCA
                                                                                                                                                                                                                                                                                                                         575;
                                   gtgcctgcggtacgacccgtcggtgcagtccaacacccggcagctcgacgtcgacgtgga
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RFWRHGKSGGSGLGLAIYQAIYQRCQCRLDFDSRADGLRVTLEMPLRC"
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No. 1.1e-09;
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                       Submitted (01-SEP-2001) Haruo Ikeda, Kitasato Microbial Chemistry, School of Pharmaceutical Shirokane, Minato-ku, Tokyo 108-8641, Japan (E-mail:ikeda@mc.pharm.kitasato-u.ac.jp, Tel:+Fax:+81-3-3444-6197)
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AB070947
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Kikuchi, H., Shiba, T.,
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Shiba,T., Sakaki,Y. and Hattori,M.
ence of an industrial microorganism Streptomyces
Deducing the ability of producing secondary
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                     CGACGGTCAATCTGATCGGCAACGGCACCCTGGCCCTGCTGCGCCACCCCGACCAACTCG
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CGTTCCACGGACTGCTGCCCGGCTGCCCGGCCTTGCGCTGTCCGTACCGCCGGAGCAGT 16188

IMPORTANT: This sequenced clone.

This sequence MAY NOT be the entire clone. It may be shorter because we

shorter because we

only sequence insert of the

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JOURNAL
MEDLINE
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http://www.nih.go.jp/
http://www.nih.go.jp/
pun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the initiation codon).
                                                                                                                                                                                                                                                                                                                                          ODS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor sequencing at The Sanger Centre is funded by the BBSRC and Beowulf Genomics

Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)

CDS are numbered using the following system eg SC7B7.01c. SC (Sceelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta o is given for content to the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match found by fasta or is given for the bighest scoring match for 
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Submitted (27-SEP-2000) Streptomyces coelicolor sequencing project,
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA E-mail: barrellsanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
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Cerdeno, A.M., Parkhill, J.,
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Unpublished
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A set of ordered cosmids and a detailed genetic and pl for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21(1), 77-96 (1996)
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Streptomyces coelicolor
AL442629
AL442629.1 GI:10432457
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cosmid H63.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complement(<1..957)

/gene="SCH63.01c"
/gene="SCH63.01c, possible ABC transport system integral /note="SCH63.01c, possible ABC transport system integral membrane protein (fragment), len: >319 aa; similar to TR:CAB77000 (EMBL:AL159178) Streptomyces coelicolor putative integral membrane protein SCH22A.31, 850 aa; fasta scores: opt: 510 z-score: 493.4 E(): 5.8e-20; 38.1% identity in 315 aa overlap. Contains possible hydrophobic membrane spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EMBL:AL161691) Streptomyces coelicolor putative ABC-transporter ATP binding protein SCD40A.12c, 246 aa; ABC-transporter aTP binding protein SCD40A.12c, 246 aa; fasta scores: opt: 1007 z-score: 1087.6 E(): 0; 67.4% identity in 236 aa overlap. Contains Pfam match to entry PF00005 ABC_tran, ABC transporter and match to Prosite entry PF00017 ATP_GTP-binding site motif A (P-loop) and PF000211 ABC transporters family signature*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PS00017 ATP/GTP-binding site motif A (P-loop)"
complement(1957. .2631)
/gene="SCH63.03c"
                                                                                                                                                                                                                           /note="Pfam match to entry PF00005 ABC_tran, ABC transporter, score 208.40, E-value 1.1e-58" complement(1245. .1289)
/gene="SCH63.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                         GTFTAVMGPSGSGKSTFLQCAAGLDRPSAGSVRLGGTEITGMNENELTELRRSRLGFV
FQAFNLLPSLTVEQNVLLPMRLAGQRQDHRRAADVLAQVGLADKARRRPGELSGGQQQ
RVAVARALVTAPDVIFADEPTGALDTGTAAEVLGLLRQAVDGLGATVVMVTHDPAAAA
complement(1957. .2631)
/gene="SCH63.03c"
                                                                                                                                           /note="PS00211 ABC transporters
complement(1572. .1595)
/gene="SCH63.02c"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SCH63.02c, possible ABC transport system ATP binding protein, len: 164 aa; similar to TR:CAB81857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(954...1748)
/gene="SCH63.02c"
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complement/os/
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/protein_id="CAC10292.1"
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/gene="SCH63.01c"
                                                                                                                                                                                                                                                                                                                                         /gene="SCH63.02c"
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/transl_table=11
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/strain="A3(2)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative ABC transport system integral membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="nominal overlap with Streptomyces coelicolor cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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                                                                                                                                                                                             family signature"
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δÃ В δÃ

Matches

26

RBS

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Query Match
Best Local
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TCTCTCTCACCGGAGGTCCCATGACCGCGCCCCACCTATGAGGAACTGGCCGCCCTGCGGG 16133
                                          tcgatcccaccgacgccgacgtgcggcgtgacccctacccgtcctaccactggctgctgc 85
                                                                                                   609;
                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sensor kinase SCH10.17c, 472 aa; fasta scores: opt: 5% z-score: 616.4 E(): 8.2e-27; 36.4% identity in 453 aa overlap. Contains possible hydrophobic membrane spanni regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="SCH63.04c, possible two component system sensor kinase, len: 448 aa; similar to TR:Q9X8Q6 (EMBL:AL049754) Streptomyces coelicolor putative two-component system streptomyces coelicolor putative two-component system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(2029. .2112)
/gene="SCH63.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Pfam match to entry PF00196 GerE, Bacterial
regulatory proteins, luxR family, score 83.30, E-value
4.9e-21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulator, len: 224 aa; similar to TR:Q9X8Q7 (EMBL:AL049754) Streptomyces coelicilor putative two-component system regulator SCH10.18c, 228 aa; fasta scores: opt: 827 z-score: 946.4 E(): 0; 62.1% identity in 219 aa overlap. Contains Pfam matches to entries PF00072
                                                                                                                                                                                                   complement(3983.
complement(3987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2628. .3974)
/gene="SCH63.04c"
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                                                                                                                                                                                                                                                                                 complement(2639.
                                                                                                                                                                                                                                                                                                   YRIYQEALANVYRHAPGAATHYSLSVARPAGGQGDGQTDGQREGPGGERLTYLVVVNEP
PPEPPAGPLEVGGTGHGLYGMRERVRLYGGTLDVGPLPDGGFRVAAQLPLTEEDIT"
                                                                                                                                                                                                                                                                                                                                                                                                         VFVADVAGALALLTVDFQERLLWPFPPMEIVGYVGLCLALGLRERRRTLLLIVWLATAG
ANVGLGFAAPHGTGAKDLLLTILGGVALLLGGALRERYEVQRRLAEQETISEAERGRR
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/db_xref="GI:10432460"
/translation="MTTRVIIYDDQAMVRAGFAALLAAQSDIDVVGEAPDGAQGVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative two component system response regulator"
                                                                                                                                                                                                                                                   /gene="SCH63.04c"
                                                                                                                                                                                                                                                                                                                                                         EMRRLLGVLRNEEAHGELVPQPGLAQIGQLVEATARTVGPVDFTGCDAEVPEAVGLSA
                                                                                                                                                                                                                                                                                                                                                                                    TLLEERARIARELHDVVAHHMSVITVQADTAEYRLAALPPDVREEFTSIAATARESLG
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/note="sch63.04c"
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ASGFLLKDAPPADLIAAVRVVASGDALLAPSVTRRLIADFAQQRPASRGKPALRLKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Pfam match to entry
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                                                                                                                        18.1%;
51.8%;
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                                                                                                                     Score 218.6; DB 1
Pred. No. 7.5e-10;
                                                                                                   Mismatches
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                                                                                                                                                                                                                              .3987)
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                                                                                                                                                DB 1;
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                                                                                                                                             Length
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        TECTECEGGGGCTGGTGGAACTGCCGGTGCGGCTC
                                                                                    GGCATCCCGCGCTCGCCGCCGGCCGGCCGGCGACGCTCACCTGGCGCACCAGCACCC
                                                                                                                gactgccgggcctgcggcttgcgcgcgtcggacgccctggcctatcagccgcgcacca
                                                                                                                                                                GCCTGGGCGCCCGCTGGGCCGCGTCGAGGCCGCCGTCGCCGTACGCCTGCTCGACC
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                                                                                                                                                                                        gcctcgggtcctacctcgcccgtacgcagctgcgccgccgcgggtggccgccctg---gccc
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                                             tgttccggggcctggccagcctgccgatcgcgttc 1194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA URGV, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arlat,M., Billault,A., Brottier,P., Camus,J.C., Cattolico,L., Chandler,M., Choisne,N., Claudel Renard,C., Cunnac,S., Demang Gaspin,C., Lavie,M., Moisan,A., Robert,C., Saurin,W., Schiex, Siguier,P., Thebault,P., Whalen,M., Wincker,P., Levy,M., Weissenbach,J. and Boucher,C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Christian.Boucher@toulouse.inra.fr
http://sequence.toulouse.inra.fr/R.solanacearum.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 190050)
Boucher, C.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Weissenbach, J. and Boucher, C.A. Genome sequence of the plant pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          segment 5/11.
AL646080 AL646053
AL646080.1 GI:17
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Ralstonia solanacearum GMI1000 r
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Gene name confidence : hypothetica
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Gene name confidence: hypothetical
predicted by Codon_usage
predicted by FrameD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plant pathogen Ralstonia solanacearum
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CDS
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Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2336. .3508)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2336.
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VIGIDASAKPEQTREQILRIARDTAKLVELGRDITEDDVVLDTRYGGPEYGLPNEGTL
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Matches
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Best Local
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acatcatcctgttccaggacgagcccgaccacggccggctgcgcgggtggtcggcccgg 304
                                                                                                                                                                     gcatccgccggttctggaccgacctcgtcgggcccgggctgctcgccgagatcgtcggcg 244
                                                            GGATGTTCCTGATGCTCAATCCGCCCATGCACACGCGCCTGCGCGGCCTGATGATGCAGG
                                                                                                                                             GCATCCGCCTGCGATACGGCGACGAAGGCCCCAACATGCCGCTGTTCCAGGGGGTTCAGCC 77625
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                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biosynthesis; isoleucine/valine"
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Gene name confidence: putative
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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complement(4302. .5198)
                                                                                                                                                                                                                                                                                                               complement(5220.
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                                                                                                                                                                                                                                                                                                                                                 NPFPGVIETAPSSRGYTGGFGTDLMLKDLGLAGDAAKSVRQPVYLGALAQQLYQASSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4302. .5198)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="small molecule metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGERIDAQTALRIGLVEEVVDTGAAREAALAMARRVTTLSPRAVTFSKALIHQARHGV
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/note="RS05574"
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(mmcQ), (mmcV),
                                                                                                                                                                                        AF127374
Streptomyces
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cytochrome P450 hydroxylase ORF3
(mitR), MitQ (mitQ), MitP (mitP), M
(mitM), MitL (mitL), MitK (mitK), M
(mitH), MitG (mitG), MitF (mitF), M
(mitC), MitB (mitB), MitA (mitA), M
                                       (mmcM),
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                                                         (mmcI),
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   MmcW
                     MmcS
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 (mmcW),
                                     MmcI
MmcJ
MmcO
               MmcO (mmcO), (mmcS), MmcT
                                                                           (mmcE),
                                                           (mmcJ),
   MmcX
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                                                                                           g, cytochrome P450 hydroxylase RF3, MitT (mitT), MitS (mitS), p), MitO (mitO), MitN (mitN), K), MitJ (mitI), K), MitJ (mitJ), MitJ (mitD), F), MitE (mitE), MitD (mitD), A), MmcA (mmcA), MmcB (mmcB),
   MmcF (mmcF), runce (mmcL),
MmcK (mmcK), MmcL (mmcL),
MmcP (mmcP), Mm

'm 'nmmcT), MmcU (mmcU), MmcV

'm 'nmmcT), MmcU (mmcU), MmcV
   (mmcX),
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                                                         (mmcF), MmcG (mmcG),
(mmcK), MmcL (mmcL),
               mcP (mmcP), MmcQ (mmcU), MmcV
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AUTHORS
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ORGANISM
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Direct Submission
Submitted (10-FEB-1999) Microbiology,
Submitted (10-FEB-1999) Microbiology,
MN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (27-MAY-1999) Microbiology, Uni. o
420 Delaware St. SE., Minneapolis, MN 55455,
Amino acid sequence updated by submitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular characterization and analysis of the cluster for the antitumor antibiotic mitomycin
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Streptomyces lavendulae
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IRYEEREEFMDMVLRLQALDATPEELGALGAENNEFMKKLAAAKRANFGDDLLSHLAH
IRYEEREEFMDMVLRLQALDATPEELGALGAENNEFMKKLAAAKRANFGDDLLSHLAH
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ITREHNPHLAFGHGIHLCLGMELARVEMRQAWRGLVTRFPGLRWAAAPEDIRWRDDQI
                                                                               DPDADPALTDLEIAGIGVLMLIAGHETSANMLGVGTYTLLENADQWALLRDDISLIDR
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/db_xref="taxon:1914"
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Firmicutes; Actinobacteria; Actinobacteridae;
Firmicutes; Actinobacteria; Actinobacteridae; Streptomyces
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ILGELVORVTGRSFRDFVTSELFAPLGLNDLHMGLPGSAWPRHVPARAAHPSEWPNOW
MSNRRGYRQAVIPSAGLSGTAAQMARFYQMLMEGGSLDGIRVLRPETVEEARKPSNDG
GIDASLKRPVRWSHGFMLGGPGPDPRGLSNVLGRTSDPSAFGHAGTTSSVVWADPTRE
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AISTVSQRITELENLRSEAVQAHIDAALELGHHQELVGELRSLTAANPLHEPPHNIQLM
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/gene="mitP"
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1 (bases 1 to 6085)

Schupp,T., Engel,N., Bietenhader,J., To STAUROSPORIN BIOSYNTHESIS GENE CLUSTERS Patent: WO 9708323-A 4 06-MAR-1997;
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Schupp, T., Engel, N., Bietenhader, J., Toupet, C.
Staurosporin biosynthesis gene clusters
Patent: US 6210935-A 403-APR-2001;
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Quorum sensing signaling in bacteria
Patent: WO 0118248-A 22 15-MAR-2001;
University of Iowa Research Foundation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-MAY-2000) Department of Medicine and University of Washington Genome Center, University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opportunistic pathogen
Nature 406 (6799), 959-964 (2000)
20437337
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AE004755.1 GI:9949456
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Box 352145, Seattle, WA 98195, (
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GEPQAQMPTASLLAQLETDDYSGSEQYRGDRAYFAEALEGLEPALFTRRRPAGLRRTA
RHRLTLERTLLDAIRDRGESPFLFLSBAVALYLARIHONDDVVLGVPVLURRDRAAKQ
VVGHFANTLPLRIRTAPEQTVDEFLAQLREATRTLLRHQKMPLGDLLRGASPLFDTTL
SYMRWPAAQAIPNASYETYAQTHAHDDPDALAIWVSEFDGHSDAQVDFEYACDVFDADF
                        PMDAAARHIETFLRALVEGGERRLGELDPLSAAEREELIHTRNATDQAFPEQATLPTL
FAEQVARTPORTALLEADGGTLSYAELDAKVQAVALKAAGVERTDERVALLVARGPH
LLPALIGVQBRAGGAVVEINDOHPLERVELLEDGGARVLLVDERAATLGESLGETRVEL
HLERLLPQSTGDLPAANVAPGDLAYVIYTSGSTGMPKGVMVEHRSVVNRLNMMORRYPI
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/gene="PA3326"
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                                                                                                                                                                                                                                                                                                             /product="probable non-ribosomal peptide
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GERDVLLQKTPVTFDVSVWELFWWSFTGARLSLLPPGAEKDPREMLRSIQRDAVTVIF
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1289. .8347
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Of Washington
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IDPDSGPLLRTVAIATDAGAHDLLVVVPHIIADGTTVLTLAEQWLTLAADPAAQPWTA
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ERWGDGPVTLLGDAAHPMLTSLGQGAAIAIEDAAVLAHCLATIDDPQAALRAYENRRR
DRARAMVETSRALSRIEQLEHPLRTVARDLYFRFAPERTFARQNELALTFPGVE"
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SALSLMPNALTALERVGVEPDLTRAQAFDSLFELTRAGFID IDEGGLAROLGOPSL
AIHHASLOQALLEOAROCREPLIELGVSATGYLHHADGEGVTVLCSDGREVHADVLTGADG
ENSAIRATMTGPERPTDMHYVIMRATPAFRHPKVTPGYVAHYMGRGQRFGLADIGEGN
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DEALLLFFYWELVWFERSDKEVEPLPEGASLEQKLDHIVERAIEAGVLPAGTPRATVQ
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MLPAFFVRIDSLPLSANGKLDRRQLPAPPEQVAAVAPRTATEAELAAVWADVLGVAEV
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RCMADARPFMAFMEAEGPINLCSSNIGRYPFPERIGALRLSDAQFLTGISVNGYFVAA
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HRELDGAQLEQLQRRAREHGTTVHGALTAALAIAAGHDHQRRPSHIAIGSPIDFRDEL
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11947 CTACGCGAAGCGTACCGGCAGCCCGCGCGCGCGAGGGGACTCAGCCACCACAT 12006
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                                           ggaccgacctcgt--
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                                                                                            CGCGCGCAAGGTCCTCAACCATCCGGGCGTCCGCCGCGACGCCCGGCAGGCCGCCGAACT
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13426. 14418
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EREHARQSWEEQAELLSPEEAQALLADAQVDYLKVLLEAKRRQPADDYYSGLVQAADES
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DGHLGYGFGYHYCVGASLARLEGRIAJQRLLAREPDLQLAVPHAELQWLPITFLRALI
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GQAVTQMADSJPLALAFDLRQGILRDGGNMVLTGFGAGLTWGSVALRWPKIVPTMD"
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YSAAQPAKEGYSDALRRELAPMGIQVSVYSPGAIWTPIWGKIASEGERALADAPDAVA
DLYRDTYLAFLQANEDGARNSAYKAPADVAAVHAALTAAKPRTRYKVGADVRRGTLLA
RLLPDSVIDGMFRPIVTAAPAAKEEQRA"
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      Streptomyces griseus genes for orf-1 and synthase and cytochrome P-450, complete complete AB018074 D45916
AB018074.1 GI:3702259
 cytochrome
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 chalcone
 synthase
                                  cds
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                                            orf-2,
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Submitted (03-0CT-1998) K
Faculty of Agriculture, D
Yayoi, Bunkyo-ku, Tokyo 1
Fax:03-3812-0544)
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LDDLCHFLDLPPEMFRYSRATLTERGNIASSVVFDALAGRF
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a 1051 c 908 g 401 t
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DIPEADREWILRAHAMTMNNVGAAGKQDAVRAKAELRGYFQELTADRRSPGEDLISTL
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ELDDRRTIPHMTFGWGAHHCLGAPLATMELEVAFSTLLTRFPALRLDVPPEDVSMNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to
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                                                                    Score 203.6; DB 1;
Pred. No. 3.4e-08;
D; Mismatches 514;
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                                                                                                                                                                          GCTGCTGACCCGCTTCCCGGCCCTGCGTCTGGACGTGCCGCCCGAGGACGTCTCGTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGCGTCGGCATCCCCCGTATCGCCCCTGGAGGACGTGGAGCTCTCCGGCGTCCTCATCAA 1272
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MITSUBLISHI RAYON CO LTD
OS Streptomyces griseus
PN JP 2000342269-A / 1
PD 12-DEC-2000
ggcgatcgccgagttcgccgactacgtggagcgggccctcgcgaggcggcgtgaggg
                                                      CGCCATGACCATGATGAACGTCGGGGCCGCGGGCAAGCAGGACGCGGTGCGCGCCAAGGC
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Streptomyces griseus
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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86; Conservative
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C C12N1:19),09,C12P7/22//C12N1/21,(C12P7/22,C12R1:19),(C12N1/21,
C12R1:19)
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/db_xref="taxon:1911"
1051 c 908 g 401 t
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Streptomyces coelicolor cosmid I
                          Direct Submission
Submitted (19-SEP-2000)
                                                                            Cerdeno, A.M., Parkhill, J.,
                                                                                                                                                      Saunders, D.C. and
                                                                                                                                                                                                                             A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
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Redenbach, M., Kieser, H.M., Denapaite, D.,
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                                                                                                      to 36028)
     SEP-2000) Streptomyces
Wellcome Trust Genome
                                                                                                                                                         Harris,
                                                                                                                                                         ò
                                                                               Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E41
coelicolor sequencing Campus, Hinxton, Cambi
                                                                                                                                                                                                                                                                                                                                       Eichner, A.,
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                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces
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                          project,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                     misc_teature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prediction is based on positional base preference in codons using specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usually the highest scoring match found by fasta o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by the BBSRC and Beowulf Genomic Details of S. coelicolor sequenc available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                upstream initiation codon.

IMPORPANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions. Cosmid E41.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            correct initiation codon. Where possible we choose an initiatic codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the matters of the company of the codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strand)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in codons is given for each CDS.
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/protein_id="CAC09533.1"
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DAAKYYNNVSREDMRFILVDAADKILPEVGFKLGQYGKEHLEGRGVEVYLSTSMDSCV
DGHYVLKNGLEYDSNTIYWTAGVKPNPALARFGLPLGFRGHVDTQATLQVQGTDYIWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"SCE41.01c, probable oxidoreductase (fragment), len:
/note-"SCE41.01c probable oxidoreductase (fragment), len:
/note-"SCE41.01c Probable oxidoreductase (fragment),
/note-"SCE41.01c Probable oxidoreductase (fragment),
/note-"SCE41.01c Probable oxidoreductase (fragment),
/note-"SCE41.01c Probable oxidoreductase"
     /clone="cosmid E41"
complement(112. .79)
/gene="SCE41.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SCE41.01c"
complemen+/
                                                                                                                                                                                                                                                               AGDNAQVPDLVGRKAGNENAWCPPNAQHALRQAKVLGDNVI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SCE41.01c"
                                                                                                         /strain="A3(2
                                                                                                                      /organism="Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:1902"
                                                                                       /db_xref="taxon:100226"
                                                                                                                                                                                                                /note="nominal
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                                                                                                                                                                                                             overlap
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                                                                                                                                      coelicolor A3(2)
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                                                                                                                                                                                                                   coelicolor cosmid
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complement(3061...3585)
/gene="SCE41.04c"
/gene="SCE41.04c, hypothetical protein, len: 174 aa;
/note="SCE41.04c, hypothetical protein, len: 174 aa;
similar to TR:P96376 (EMBL:Z92539) Mycobacterium
tuberculosis hypothetical 24.6 kDa protein MTC10G2.25c,
228 aa; fasta scores: opt: 273 z-score: 332.6 E():
5.1e-I1; 35.6% identity in 149 aa.overlap. Contains
possible coiled-coil region at approx residues 87...106
    /note-"SCE41.05c, eno, enolase, len: 426 aa; similar to SW:ENO_ECOLI (EMBL:X82400) Escherichia coli enolase (EC 4.2.1.11) Eno, 431 aa; fasta scores: opt: 1603 z-score: 1807.6 E(): 0; 60.6% identity in 419 aa overlap. Contain Pfam match to entry PF00113 enolase, Enol-ase and match
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/db_xref="GI:10241777"
/translation="MQTPPPTTPRTEPTDADVAAFKQQLGRPPRGLRAIAHRCPCGQP
/translation="MQTPPPTLYYLTCPKAASAIGTLEANGVMKEMTERLATDPELAAAYRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SCE41.03c, conserved hypothetical protein, len: 1 aa; similar to TR:P96375 (EMBI:.292539) Mycobacterium tuberculosis hypothetical 16.6 kDa protein MTCY10G2.24c, 155 aa; fasta scores: opt: 632 z-score: 730.7 E(): 0; 67.6% identity in 136 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SCE41.02c, possible hydrolase, len: 313 aa; similar to N-terminal region of SW:GPPA_ECOLI (EMBL.M87049)
Escherichia coli guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase (EC 3.6.1.40) GppA, 494 aa; fasta scores: opt: 311 z-score: 357.2 E(): 2.2e-12; 28.48 identity in
                                                                                                                                           complement(3639. .4919)
                                                                                                                                                                                                             complement(3639. .4919)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSVTTVSAIAQELPEYDSAAIHHSRVSRDRVREITDWLLASTHAERAAVASMHPGRVD
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VDVGCVRMTERHLVRDGAVTDPPTAEQVAAMRADIEAALDLAGRTVPLGEARTLVGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative hydrolase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1477. .2418)
/gene="SCE41.02c"
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                                                                                                                                                                                                                                  WDGVDKADAVARRQ"
                                                                                                                                                                                                                                                     LRDLKARWQDDAYAEQQVRLRLHYVMPGETGFVVVDPEAAEQTRARAGAADRPWYQNV
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complement/2007
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complement/^^^
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                                                                                                                                                                /note="SCE41.05c"
                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
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/note="SCE41.03c,
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Best Local
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  aggcggcggcgtgag-----
                                                                  GCCCGGTCGGTGAAGAAGATGCGCGGCTACCTCGCCGACCTCATCCACCGCAAGCGCGCC
                                                                                                atgcgccgcggccacgcgatcgccgagttcgccgactacgtggagcgggccctcgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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ggcggcgaggacctgctggcgttgatgctcgacgcc
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1 gtgctggtcgatgccgtgaccgcgttcgatcccaccgacgccgacgtgcggtgacccc 60
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                                      gtcgggcgctggtcgcgcgacgttgggacggaccctggaccggggcgccagcgccgaggac 540
                                                                                                                           CCGCTGCCCATCTACGCCATCTGCGACCTGCTCGGCGTCCCCCGCGAGGACCAGGACGAC
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complement(5181. .5915)
/gene="SCE41.06c"
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KGSLGANAILGVSLAVAHAASEASDLPLFRYLGGPNAHLLPVPMMNILNGGSHADSNV
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/note="PS00164 Enolase
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LDLILEAIKEAGYTPGEQIALALDVAASEFYKDGSYAFEGKNRSAAEMTEYYAELVEA
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Cytochrome P-450.

Streptomyces antibioticus (tissue library: ATCC 11891) DNA.

Streptomyces antibioticus

Streptomyces antibioticus

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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Rodriguez, A.M., Olano, C., Mendez, C., Hutchinson, C. A cytochrome P450-like gene possibly involved in o blosynthesis by Streptomyces antibioticus FEMS Microbiol. Lett. 127 (1-2), 117-120 (1995)
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Streptomyces antibioticus
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DELDFHRERNPH 1AFGHGAHHCIGAQLGRUELQEALSALVRRFPTLDLAEEVVAGLKWK
QGMLIRGLERQIVSW
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                                                   1103 tgccgggcctgcggctggggctgcgcgtcggaccgctggccttatcagccgcgcaccatgt 1162
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Search completed: June 21, 2002, 15:52:22 Job time: 7353 sec

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibiotics, anti-inflammatory agents, anti-cancer agents, immune-enhancers, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other disease involving respiratory inflammation, or cholesterol-lowering agents or as crop protection agents (e.g. fungicides or insecticides) as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising a mitomycin biosynthetic gene operably linked to a promoter, and host cells transformed with the cassette. The nucleotide, and protein sequences and the transformed host cells of the invention result in antiasthmatic, antiinflammatory, cytostatic, immunomodulatory, and antibiotic activities. The nucleotide sequences are used to elucidate the
                                                                                                                                                                                                                                                                  8612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB32485-B32542 represent mitomycin biosynthetic gene cluster DNA sequences and encoded proteins. Sequences AAC55812-C55814, AAC55850-C55856 and AAC55862-C55869 represent PCR primers used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 molecular basis for the biosynthesis of the mitosane ring system, as as to engineer the biosynthesis of novel natural products, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 26; Figure 22; 399pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid molecule comprising mitomycin biosynthetic gene cluster useful for cloning mitomycin biosynthetic genes for elucidating the molecular basis of mitosane ring system biosynthesis -
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            amino benzoquinone and axiridine ring systems. The S. lavendulae mitomycin biosynthetic gene cluster comprises 47 mitomycin genes spanning 55kb of DNA. The invention includes an expression cassette comprising a mitomycin biosynthetic gene operably linked to a promoter, and host cells transformed with the cassette. The nucleotide, and protein sequences and the transformed host cells of the invention result in antiasthmatic, antiinflammatory, cytostatic, immunomodulatory, and antibiotic activities. The nucleotide sequences are used to elucidate the molecular basis for the biosynthesis of the mitosane ring system, as well as to engineer the biosynthesis of novel natural products, e.g.
                                                                                                                                                                                                                                        AAB32485-B32542 represent mitomycin biosynthetic gene cluster DNA sequences and encoded proteins. Sequences AAC55812-C55814, AAC55850-C55856 and AAC55862-C55869 represent PCR primers used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to isolated and purified nucleic acid from the mitomycin biosynthetic gene cluster. Mitomycins are natural products that contain a variety of functional groups,
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The present sequence represents the 6.5kb PvuII fragment of Streptomyces longisporoflavus R19 which is involved in the biosynthesis of indole-carbazole alkaloids (ICA). The sequence contains five functional
                                                                                                                                                   Indole-carbazole alkaloid coding for the antibiotic
                                                                                                                                                                                                                                                          Bietenhader J,
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Ca2+/phospholipid-dependent serine/threonine protein kinase;
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"Partial sequence for gene 5; full length
protein contains 366 amino acids and is
significantly similar to amino transferase
enzymes, such as the Dnr J protein"
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25; Conservative
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                                                                                           Bacteria signal to one another to coordinate expression of specific genes in a cell density dependent fashion. This "bacterial signalling" is called "quorum sensing and response". Quorum sensing allows a bacterial species to sense its own number and regulate gene expression according to population density. The present sequence is an open reading frame (QRF) of a Pseudomonas aeruginosa quorum sensing controlled gene. Inhibitors of quorum sensing signalling renders a bacterial population more susceptible to treatment. The present invention relates to a method for identifying modulators of quorum sensing signalling in Pseudomonas aeruginosa bacteria. Modulators of quorum signalling in Pseudomonas aeruginosa bacteria. Modulators of quorum signalling may be used to treat P. aeruginosa infections. P. aeruginosa is an opportunistic pathogen of immunocompromised individuals (burn patients, cystic fibrosis patients, patients undergoing immunosuppressive therapy and patients with AIDS).
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                                                                                                                                                                                                                                                                                                                                            Identifying modulators of quorum sensing aeruginosa bacteria, useful for treating
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Matches 586; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparation of pyran-2-one derivative, used as intermediate and additive for thermosensible transfer paper, comprises contacting carbonyl compound with microbe containing polyketide synthase ge
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Streptomyces griseus

actinomycetes polyketide

synthase

encoding

AAF81954; 18-JUN-2001

(first entry)

AAF81954 standard;

DNA;

2795 BP

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Query Match
Best Local Similarity
Matches 586; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method for preparing 1,3,6,8-tetrahydroxynaphthalene comprising using a microbe cell containing an rppA gene encoding actinomycetes polyketide synthase, to convert malonyl CoA as the substrate or a substance which can produce malonyl CoA in the microbe cell to 1,3,6,8-tetrahydroxynaphthalene and recovering it. 1,3,6,8-tetrahydroxynaphthalene is used as a synthetic material for melanine and as an intermediate for drugs and agricultural chemicals. The present sequence encodes the actinomycetes polyketide synthase protein isolated from Streptomyces griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
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1,3,6,8-tetrahydroxynaphthalene; melanine; agricultural chemical;
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0; Mismatches
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pks; tvpe I; 8,8a-deoxvoleandolide synthase; modular; ketosynthase;
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                                                                                                                                    PKS; type I; 8,8a-deoxyoleandolide synthase; modular; acyl-transferase; acyl carrier protein; inactivated; macrolactone; antibiotic; motilide; erythromycin; ss.
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The cleanfolide polyketide synthase (PKS), also known as 8,8a-deoxyoleanfolide synthase, is encoded by three open reading frames (ORF), designated oleAI, cleAII and cleAII. The PKS is a type I "modular" enzyme, where each ORF encodes 2 extender modules and the first ORF also encodes the loading module. Each module is composed of at least a ketosynthase (KS), acyl-transferase (AT) and an acyl carrier protein (ACP) domain. The cleanfolide PKS loading module contains an inactivated KS, called KS-Q, where Q is the abbreviation for glutamine, present instead of the active site cysteine required for
glutamine, present instead of the active site cy
activity. The large multifunctional PKS enzymes
of polyketide macrolactones through multistep pa
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                                                                                                                                                                        loading module or any one of extender modules
                                                                                                                          is part of the Streptococcus antibioticus oleandomycin gene cluster
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/label= oleP1
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/product= 8,8a=
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                                                  Matches
                                                                      Query Match
Best Local Similarity
                                                                                                                                                                     Sequence 50937 BP; 6672 A; 16253 C; 19272 G; 8740 T;
    86
                                                592;
                                                  Conservative
                                                                      16.2%;
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Pred. No. 5.3e-19;
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                 /rag h
/product "ORF 33 |
12251..13399
                                                                                                                                                                                                                                                                                                                                biosynthesis
                                                                                                                                           /product= "P450 hydroxylase" complement (6628..7734)
                                                                                                                                                                                                                                                                    Location/Qualifiers complement (1..632)
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complement (5539..10361)
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5249..6505
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/product= "transmembrane
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                                                                                                                                                                                                                                               product= "type II NRPS adenylation enzyme"
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                                                    1261..12094
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Query Match
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Matches 604
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                                                                                                                                  The present sequence is the last 21184 bases of the enediyne C-1027 gene cluster from Streptomyces globisporus. Enedlyne C-1027 is an antibiotic, consisting of an apoprotein and a non-peptidic chromophore, which acts by damaging DNA. The sequences within the gene cluster, and the proteins they encode, can be used in the treatment of cancer, along with antagonists of the protein. Each of the open reading frames is specifically claimed, excluding ORF 9, which encodes CagA.
                                                                                                                                                                                                                                                                                                                                                                             Shen
                                                                                                                                                                                                                                     Claim 1; Page 130-157; 160pp; English.
                                                                                                                                                                                                                                                             Isolated nucleic acid comprising a nucleic acid encoding any open reading frames (ORFs) -7 to 42, excluding ORF 9 (cagA), the production of enediyne C-1027 antitumour antibiotics -
                                                                                                                                                                                                                                                                                                              P-PSDB; AAB13588, AAB13589, AAB13590, AAB13591, AAB13592, AAB13593, AAB13594, AAB13595, AAB13596, AAB13597, AAB13598, AAB13600, AAB13601, AAB13602, AAB13603, AAB13607, AAB13606.
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05-JAN-2000;
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           44 acgtgcggcgtgacccctacccgtcctaccactggctgctgcggcacg---acccggtgc 100
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aggggcgtcaggacccctatcccttctacgaggcgatccgcgcgcacgggcaggcggtcc 5363
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/product= "ORF 41 protein"
complement (20807..21185)
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complement (18112..18642)
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Pred. No. 7.9e-19;
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cancer; ds.
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complement (16653..17924)
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complement (14690..15922)
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13012..14079
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complement (11351..12835)
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complement (7573..9900)
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                                                                                                                                                                                                                                                                                        /*tag=
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complement (9982..11349)
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/product= "ORF -3 protein'
5982..7479
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/product= "0-acyl transferase"
complement (24986..25564)
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29632..31197
/*tag- y
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/transl_except= (pos:35226..35228.aa:Ala)
complement (35518..35938)
/*tag= ac ______/*tag= ac ______/*tag= ac _____/*tag= ac ____/*tag= ac ___//*tag= ac ____//*tag= ac ___//*tag= ac __//*tag= ac ___//*tag= ac __//*tag= 
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27214..28593
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/*tag= ak
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43945..46024
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/product= "aminomutase"
complement (41052..42611)
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28590..29588
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25815..27170
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/product= "ORF 34
56026..56880
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/product= "transmembrane transport
46167..47171
/*tag= aj
/product= "O-methyl transferase"
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/product= "coenzyme F390 synthetase"
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/product= "ORF 33
54231..55379
                                                                                                                                                                                                                                     /product= "ORF 31 protein" complement (51421..52341)
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/product= "oxidoreductase"
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50350..51390
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complement (39367..40986)
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/product=
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duct= "coenzyme F390 synthetase"
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                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is the enediyne C-1027 gene cluster from Streptomyces globisporus. Enediyne C-1027 is an antibiotic, consisting an apoprotein and a non-epetidic chromophore, which acts by damaging DN The sequences within the gene cluster, and the proteins they encode, ce be used in the treatment of cancer, along with antagonists of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAB13554, AAB13555, AAB13556, AAB13557, AAB13558, AAB13559, AAB13560, AAB13561, AAB13562, AAB13563, AAB13564, AAB13565, AAB13566, AAB13567, AAB13568, AAB13569, AAB13570, AAB13571, AAB13572, AAB13573, AAB13574, AAB13575, AAB13576, AAB13577, AAB13577, AAB13579, AAB13578, AAB13574, AAB13575, AAB13576, AAB13578, AAB13580, AAB13581, AAB13582, AAB13583, AAB13583, AAB13583, AAB13583, AAB13583, AAB13584, AAB13589, AAB13590, AAB13591, AAB13592, AAB13593, AAB13594, AAB13595, AAB13596, AAB13597, AAB13598, AAB13600, AAB13601, AAB13602,
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05-JAN-2000;
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                                       aaccggccctgcgcgtccaggacgccaggagctacgacgtcgtcttcccctcgtggcggt 47462
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    cgggctgctc-gccgagatcgtcggcgacatcatcctgttccaggacgagcccgaccacg
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604; Conser
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/product= "
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complement (62787..63164)
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62045..62899
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Matches Query Match Best Local

Local Similarity es 571; Conser

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cc antiasthmatic, antiinflammatory, cytostatic, immunodulatory, and cantiblotic activities. The nucleotide sequences are used to elucidate the cmolecular basis for the biosynthesis of the mitosane ring system, as well cas to engineer the biosynthesis of novel natural products, e.g. antibiotics, anti-inflammatory agents, anti-cancer agents, chronic commune-enhancers, immunosuppressants, agents to treat asthma, chronic constructive pulmonary disease as well as other disease involving crespiratory inflammation, or cholesterol-lowering agents or as crop crotection agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents (e.g. fungicides or insecticides) as well as composition agents 
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     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to isolated and purified nucleic acid molecules from the mitomycin biosynthetic gene cluster. Mitomycins are a group of natural products that contain a variety of functional groups, including amino benzoquinone and axiridine ring systems. The S. lavendulae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid molecule comprising mitomycin biosynthetic gene cluster useful for cloning mitomycin biosynthetic genes for elucidating the molecular basis of mitosane ring system biosynthesis
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chronic obstructive pulmonary disease; respiratory inflammation;
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Query Match Best Local Matches

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RESULT :
 Cytochrome P450soy was purified from S.griseus ATCC 13273. Two CC similar forms of P450soy were isolated. P450soy-delta, is derived CC from P450soy by in vitro proteolysis during isolation. One of the Ctryptic peptide fragments of cytochrome P450soy and of of the CC P450soy-delta protein were subjected to automated degradation. The CC N450soy-delta protein were subjected to automated degradation. The CC N450soy-delta protein were subjected to automated degradation. The CC N450soy-delta protein were subjected to automated degradation. The CC N450soy-delta protein were subjected to automated degradation. The CC N450soy-delta protein were subjected to automated degradation. The CC N450soy-delta protein peptide was made. It consists of the Sequences in Q43290-23. The Oligo mixture was end-labeled and used CC to probe the EMBL4 library of S.griseus DNA. Hybridising plaques CC were isolated and a 4.8kb Saci DNA fragment was isolated from one CC clone that hybridised to the Oligo probe mixture. As segment of the CC 1.8kb fragment was sequenced and found to contain an ORF. Within CC this ORF was a section that corresp. exactly to the AA sequence CC determined from the cytochrome P450soy protein was called soyC. Five C nucleotides downstream from the stop codon for soyC another ORF was cidentified. This ORF encodes an apparent ferredoxin-like protein.

CC The gene was designated soyB and the protein ferredoxin-soy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New 6-deoxy:erythromycin derivs. - are antibiotics with increased acid stability, produced by cultivation of saccharopolyspora.
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P-PSDB; AAR14724.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, wycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and H37RV (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic monitoring
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New recombinant pick hydroxylase gene of Streptomyces venezuelae useful for converting ketolides to antibiotics and as antibiotics and intermediates in the synthesis of compounds with pharmaceutical value
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Columns 41-44; 117pp; English.

production of narbonolide, narbonolide derivatives and polyketides that are useful as antibiotics and as intermediates in the synthesis of compounds with pharmaceutical value. The DNA compounds may also encode a C12-hydroxyalse (picK), desosamine biosynthesis and desosaminyl transferase enzymes (useful for conversion of ketolides to antibiotics), and the beta-glucosidase enzyme (involved in picromycin biosynthesis). These compounds are also useful for increasing the antibiotic activity of a compound relative to the unhydroxylated compound. The recombinant host cells are useful as genetic systems that allow rapid engineering of the narbonolide polyketide synthase. These would be valuable for creating nown to the proposed to the systems that allow rapid engineering contents of the narbonolide polyketide synthase. expressing production creating of the present sequence is used to produce the recombinant DNA compounds the invention. The specification describes a recombinant DNA compound ressing recombinant polyketide synthase genes in host cells for the duction of narbonolide, narbonolide derivatives and polyketides that novel ketolide analogs for pharmaceutical applications

Sequence 5970 BP; 806 A; 2219 C; 2142 G; 800 T; 3 other;

Query Match
Best Local Similarity
Matches 600; Conser

Conservative

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45;

Gaps

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14.8%;

Score 179; DB 21; Pred. No. 1.3e-16;

Length 5970; Indels

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11,	Sequence 30, App	Sequence 1, Appl	Sequence 1, Appl	Sequence 1, Appl	Sequence 5, Appl		Sequence 1, Appl	Sequence 1, Appl:	Sequence 1, Appl:	Sequence 4, Appl:	Sequence 4, Appl	Sequence 7, Appl	Sequence 7, Appl:	•	`	•	`

ALIGNMENTS

Sequence 4, Application US/09029603 Patent No. 6210935 GENERAL INFORMATION: CURRENT APPLICATION NUMBER: US/09/029,603 CURRENT FILING DATE: 1998-03-20 EARLIER APPLICATION NUMBER: PCT/EP96/03643 EARLIER FILING DATE: 1996-08-19 NUMBER OF SEQ ID NOS: 11 SOFTWARE: Patentin Ver. 2.0 APPLICANT: Schupp, Thomas APPLICANT: Engel, Natalie APPLICANT: Betenhader, Jurg APPLICANT: Toupet, Christine APPLICANT: Toupet, Christine APPLICANT: Posplech, Andreas TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters FILE REFERENCE: 4-20555/A/PCT NAME/KEY: misc_RNA LOCATION: (5071)..(6085) OTHER INFORMATION: ORF NAME/KEY: misc_RNA LOCATION: (4013)..(4999) OTHER INFORMATION: ORF FEATURE: NAME/KEY: misc_RNA LOCATION: (1747)..(2553) NAME/KEY: misc_RNA LOCATION: (378)..(1665) OTHER INFORMATION: ORF ORGANISM: Streptomyces longisporoflavus FEATURE: NAME/KEY: misc_RNA LOCATION: (2593)... OTHER INFORMATION: ORF OTHER INFORMATION: ORF .(4011)

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APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE PO:
FILE REFERENCE: 30062-20029.00
CURRENT APPLICATION NUMBER: US/09/428,517
CURRENT FILING DATE: 1999-10-28
EARLIER APPLICATION NUMBER: 60/120,254
EARLIER FILING DATE: 1999-02-16
EARLIER APPLICATION NUMBER: 60/106,100
EARLIER FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
IENCTH. 50027
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Pred. No. 5.3e-24;
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US-08-102-863-10
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                                TELEFAX: 302-892-7949
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/102,86
                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: GALLEGOS, R. THOMP
                   SEQUENCE CHARACTERISTICS:
                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-7342
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                         NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: CR-9000
                                                                      TELEPHONE:
                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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ADDRESSEE: AND COMPANY
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; STRANDEDNISS: singl
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (0
US-08-102-863-10
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Pred. No. 1.1e-23;
0; Mismatches 507;
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GENERAL INFORMATION:
APPLICANT: SARIASLANI, SIMA
                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 1735 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 1.0 MB
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10885
FILING DATE: 19921216
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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COMPANY
CITY: 1007 MARKET STREET
STATE: DELAWATE
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REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: CR-
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                                                     GACGGACGCCCGGTCTGGGCGTCACCGGGCACGCCCTGGCCCGTCGGCTACTGGCGGAC 402
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nilarity 51.4%;
Conservative
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EXPRESSION OF P450SOY
AND FERREDOXIN-SOY IN
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Pred. No. 1.1e-23;
0; Mismatches 507;
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 RESULT 5
US-09-103-840A-2/c
; Sequence 2, Application
; Patent No. 6294328
; GENERAL INFORMATION:
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LENGTH: 4403765
TYPE: DNA
                                                                                3947465 GTTGCTGCCCGGGGCCATCGAGGAGATGCTACGTTGGACCGCCCCGGTAAAGAACATGTG 3947406
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENYER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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                                  ccggcagctcgacgtcgacgtggagctgcgggtcggcggctgcgccgcgacgacgtcgt 926
                                                                                                                                                                      TGGTACCGAGCAGCTGCTGCGCAACCGTGACCAGTGGGACCTGCTGCAGCGCGACCCGTC 3947466
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US-09-320-878-21
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NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 21
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Best Local Similarity
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APPLICANT: BETLACH, Mary C.
APPLICANT: McDaniel, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
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GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Yee, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and
FILE REFERENCE: 600. 438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 38
LENGTH: 1251
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Best Local Similarity 51.9%;
Matches 599; Conservative
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Pred. No. 4.8e-21;
0; Mismatches 511;
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FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
SEQ ID NO:17:
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APPLICANT: DEAN, CAROLINE;HARDER, PATRICIA A.;LETO, KENNETH; J.; O'KEEFE, DANIEL P.;OMER, CHARLES A.;ROMESSER, JAMES A.;TEPPERMAN, JAMES M.
TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING;
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Best Local Similarity
Matches 612; Conserv
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CURRENT APPLICATION DATA:
US/07/569,781
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FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
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Pred. No. 5.6e-21;
0; Mismatches 545; Indels 4
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ОУ	Db -	Qy	D Qy	뮹	QУ	DЪ	Qy	DЬ	Qy	В	Qу	DЪ	Qy	Db	Qy	Db	Qy	Вb	Qy	Db	Ωу	Db	Qy	ДЪ	γ	Db	Qу	DЬ	VΩ	Db
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cgcgt 1192 	cacyaygayatcccyttccycygcyacatygcyatctacyyyytccactcyctyccyat 12	toggacgccctggcctatcagccgcgcaccatgttccggggcctggccagcctgccgat 1	gctgcgcgcgcggtggccgccctggcccgactgccgggcctgcgctgggctgcgc 1127	ccacgtggccttcggcttcgcgtccaccagtgcctgggacagccgttggccagggtgga 1082	gtccttcggcgcggggatgcgctactgcctcgggtcctacctcgcccgtac	ccgggacgccgaggtfttccccggcggcgacgacctcgacgtggcccgcgacgccgccgcg 1022	cgggacccgcggcggtacgaccggcccgacgatttcgacatcgagcgggatccggtc	cggcggcaccatcgccgccggcgaggcgtcctgtgcatgatcagct	ytoggoggotgogoogaogaogtogtogtoottggooggoo	acaacggcgtt	tgcggtacgacccgtcggtgcagtccaacacccggcagctcgacgtcgacgtgga 89	cyaccaactcgcccgyctgcycgccyaacccycgctcytcaagggcyccytcyaggagct 842	gccggccggacctgctggcccaggccgtcgagga	cggccacgagacgaccgccaacatgaccgcgctctccaccctcgtgctgctgcgcgaaccc 782	aggtgggcaacgccgtgctgagcctgct;	cgcggcgagctcgacgacacccagatcgccaccatgggacgcctgttgctggtc	gaccgcggcctgatgagtcgcaacgagatcgtcagcacggtggtcacgttcatct		ctcgcgaggcggcgtgagggcggcgaggacctgctggcgttgatgctcgacgcc	ogaggaagtccgggccgcccaggacgagttgctggagtacctcgcccggctcgcccggac 620	gaggacatgogocgogocacgoggogatogocgagttogocgactaogtggagoggg	cgcgttcttccaggagcgcagcgggtcctgtcaccctgcggtccactcc 560	cggaccctggaccggggcgccagcg	gctgccgctgccgtccctggtga	tecteggeetgeteggeetgeeeg	cgacgacctggtcgaccggatgaccaccgggacgcacctccgccgacctggtcaccgagtt 449	gacgacctgctgcggcccgccctggcccggggggcgcgatggacgtggtcgacgagc		99	

RESULT 9
5212296-8
;Patent No. 5212296
;APPLICANT: DEAN, CAROLINE;HARDER, PATRICIA A.;LETO,
; APPLICANT: DANIEL P.;OMER, CHARLES A.;ROMESSER, JAMES
;J.; O'KEEFE, DANIEL P.;OMER, CHARLES A.;ROMESSER, JAMES

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APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
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; TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
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Best Local Similarity
Matches 611; Conserv
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CURRENT APPLICATION DATA:
   917
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APPLICANT: DEAN, CAROLINE;HARDER, PATRICIA A.;LETO,
;J.; O'KEEFE, DANIEL P.;OMER, CHARLES A.;ROMESSER, JAMES
;TEPPERMAN, JAMES M.
TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOL:
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APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
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CURRENT APPLICATION DATA:
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FILING DATE: 23-AUG-1990
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RESULT 11
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;Patent No. 5212296
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; APPLICANT: DEAN, CAROLINE;HARDER, PA;
;J.; O'KEBEE, DANIEL P.;OMER, CHARLES A.;
;TEPPERMAN, JAMES M.
: TITLE OF INVENTION: EXPRESSION OF F
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PILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
PILING DATE: 12-JAN-1990
APPLICATION UMBER: 405,605
FILING DATE: 11-SEP-1989
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Pred. No. 8.9e-18;
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RESULT 12
US-08-765-907A-9
Sequence 9, Application U/
Sequent No. 6352839
Patent No. 6352839
CENERAL INFORMATION:
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APPLICANT: THIBAUT, Denis
APPLICANT: BAMAS-JACQUES, Na
APPLICANT: BLANCHE, Francis
APPLICANT: COUZET, Joel
APPLICANT: BARRIERE, Jean-Cl
APPLICANT: DEBUSSCHE, Lauren
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Best Local :
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LENGTH: 1194
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APPLICANT:
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ORGANISM: Streptomyces
-08-765-907A-9
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TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
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NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.0
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DUTRUC-ROSSET, Gilles
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DEBUSSCHE, Laurent
FAMECHON, Alain
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COUZET, Joel
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                                                                                                                                 Patent No. 6352839
GENERAL INFORMATION:
APPLICANT: BLANC, Veronique
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                                                                            THIBAUT, Denis
BAMAS-JACQUES, Nathalie
BLANCHE, Francis
COUZET, Joel
                                   BARRIERE, Jean-Claude
DEBUSSCHE, Laurent
FAMECHON, Alain
            PARIS, Jean-Marc
DUTRUC-ROSSET, Gilles
Streptogramins
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; TYPE: DNA
; ORGANIZM: Streptomyces pristinaespiralis
US-08-765-907A-6
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 17
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Pred. No. 1.9e-15;
0; Mismatches 496;
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; TOPOLOGY: 1; MOLECULE TYPE: US-09-385-028-23
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US-09-385-028-23
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TITLE OF INVENTION: Acid Biosynthesis
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Patent No. 6232106
                                                                                                                       TELEX: RCA 248593 IDEA UR INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                         PILING DATE: 29-DAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. DOUGLAS Price
REGISTRATION UNMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Bullding, 400 Seventh Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
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CITY: Washington
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TELEPHONE: (202) 39305350
TELEPHONE: (202) 39305350
                                                  STRANDEDNESS:
                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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29-JAN-1997
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Query Match Best Local (Matches

Local Similarity hes 513; Conserv

Conservative

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Score 137.4; DB 4 Pred. No. 1.2e-14; 0; Mismatches 471

DB 4;

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RESULT 15 US-09-385-028-1

Sequence 1, Application US/09385028

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Patent No. 6232106
GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence
Patent No. 6232106
Patent No. 6232106
Patent No. 6232106
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Best Local Similarity
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TELEFAX: (202) 39305350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                       13957
                                                                                                                                    14017
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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HYPOTHETICAL: NO
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TYPE: nucleic acid
STRANDEDNESS: single
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Search completed: June 21, 2002, 17:04:32 Job time: 9412 sec

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90.8	91	91	91	91.2	91.2	91.4	91.4	91.4	91.6	91.6	91.6	91.6	91.8	92.2	92.6	92.6	93	93.2	93.4	93.6	93.6	93.8	94	94.2	94.4		94.8
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1123	1598	1299	992	1387	1085	1538	1520	1232	1669	1542	932	918	990	925	986	907	1231	1138	1121	1366	1165	1250	965	1244	1126	1452	1328
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AG080476	AG030579	AG039481	AG057280	AW731151	AG152796	AG030607	AG057334	AG072425	AG072737	AG032943	CNS0072Q	AG043040	AG043619	CNS0091P	AG074680	BG846266	AG064011	AI374006	AG062320	AG065058	AG030649	AG043469	AQ893417	BG846745	AG064051	AG032979	AG043615
Pan	Pan	Pan	Pan	GA	Pan	Pan	Pan		Pan		AL066742 Drosophil		_	AL053013 Drosophil			AG064011 Pan troql	SWOV	Pan	Pan	Pan			1024	Pan		AG043615 Pan trogl

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                                                      source
                                                                                                                                                                                                                                                   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (SSC); 1-7-22 Suchiro-chou, Tsuruni-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tal:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 1798)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS; GSS (genome survey sequence).
Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-040F09.TJ.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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AG171124
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                                                                                                     Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
                                                      1. .1798
                                                                         Location/Qualifiers
/organism≃"Pan troglodytes"
/db_xref="taxon:9598"
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ne: RP43-040F09.TJ, genomic
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/sex="male"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
a 778 c 655 g 0 t 365 others
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Direct Submission
Submitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC ence are derived during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Pan troglodytes male lymphoblast DNA,
BAC Library clone:PTB-047106.F.
Pan troglodytes
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GSS; GSS (genome survev
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R.Site 2 : SacI
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                                                                                                                                                                                                                             /sex="male"
/cell_type="lymphoblast"
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/clone_3 c 533 g 33 t 1
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/db_xref="taxon:9598"
/clone="PTB-047106.F"
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46.7%;
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                                                                                                                           Score 104.8; DB 1
Pred. No. 0.00053;
0; Mismatches 441
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124 others
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N Pan troglodytes DNA, clone: PTB-007004.F
AG032979
AG032979.1 GI:16559852
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone:PTB-007004.F.
                                                                                                                                                                                                                                    gc-tgcgccgcgacgacgtcgtggtcgtcctggccggcggcggcgaaccggggacccgcgggc
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                           Fujiyama, A., Hattori, M., To
Totoki, Y., Watanabe, H. and
                                                      Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                         Pan troglodytes
                                              (sites)
                                                                                                                                                                                                         975
                                                                                                                                                                                       417
                                                    Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Pan.
                           Toyoda,A., Taylor,T.D., Yada,T..
                                                                                                                               2 bp DNA
PTB-007004.F,
                                                                                          clone_lib:PTB
                                                                                                                               genomic
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                                                                                         Chimpanzee
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                             accgacctcgtcgggcccgggctgctcgccgagatcgtcggcgacatcatcctgttccag
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                                                                                                                                                                                                                                                                                    gacgagcccgaccacggccggctgcgcggggtggtcggcccggcgttctcgccgtccgcg 321
                                                                                                                                                                                                               Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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R.Site 1 : SacI
R.Site 2 : SacI.
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/clone_lib="PTB Chimpanzee Male
/s81 c 600 g 74 t J
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/sex="male"
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/db_xref="taxon:9598"
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Pred. No. 0.00084;
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cctcgtcgggcccgggctgctcgccgagatcgtcggcgacatcatcctgttccaggacga
                                                          gogogoggtgotoggogagogottogocoggacoggcatocgcoggttotggacoga 206
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                                    ececececececece-ceccececececesengecegnengcececececececece
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Totoki,Y., Watanabe,H. and Sakak
BAC end sequences of Library PTB
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Totoki,Y., Watanabe,H. and Sakaki,Y
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GSS; GSS (genome survey
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R.Site 2
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657 c 614 g 19 t 191 others
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/db_xref="taxon:9598"
/clone="PTB-007N10.F"
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45.9%;
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Pred. No. 0.0012;
0; Mismatches 590;
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BG809984/c LOCUS

DEFINITION

BG809984 1516 bp mRNA linear mgct002xd11f Magnaporthe grisea Appressorium Stage grisea cDNA clone mgct002xd11f 5', mRNA sequence.

CDNA

22-MAY-2001 Magnaporthe

ACCESSION VERSION KEYWORDS

grisea cDNA clone BG809984 BG809984.1 GI:141

GI:14180964

SOURCE

Magnaporthe

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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ralph_dean@ncsu.edu
Seg primer: T3 primer (AATTAACCCTCACTAAAGGG).
Location/Qualifiers
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North Carolina State University
Campus Box 7251, Raleigh, NC 27895,
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a 657 c 660 g 16 t 118 others
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/clone="mgct002xd11f"
/clone="mgct002xd11f"
/clone="mgct002xd1f"
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/strain="70-15"
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                                                                                                                                                                                                                                                                                          Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695,
Tel: 919-513-0020
Fax: 919-513-0024
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        Site_2: XhoI; The appressorium formation-specific cDNA library was constructed from conidia germinated for 5-8 hr on an inductive surface. The library contains over 55,000 clones with average insert size of 1.5 kbp."

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                                                                                                           /db_xref="taxn:148305"
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                                                      gaccagctcgacctgctccggcgccggccggacctgctggcccaggccgtcgaggagtgc
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Pred. No. 0.0016;
0; Mismatches 624;
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catccgccggttctggaccgacctcgtcgggcccgggctgctcgccgagatcgtcggcga 245
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AG077201
AC077201.1 GI:16629003
GSS; GSS (GERRAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC encas generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS; GSS (genome survey sequence).

Pan troglodytes male lymphoblast DNA, clone_lib:PTB
BAC Library clone:PTB-071K05.F.

Pan troglodytes
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone tracking errors.
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nilarity 46.2%;
Conservative
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R.Site 2
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                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9598"
/clone="PTB-071K05.F"
/sex="male"
                                                                                                                                                                                                                                                                                                                              /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male
549 c 663 g 15 t
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1. .1309
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Pred. No. 0.0025;
0; Mismatches 572;
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35 others
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GSS; GSS (genome survey s
Pan troglodytes male lymp
BAC Library clone:PTB-003
Pan troglodytes
GSS (genome survey sequence).
troglodytes male lymphoblast DNA,
Library clone:PTB-003A20.F.
troglodytes
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clone: F
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PTB-003A20.F,
                   clone_lib:PTB Chimpanzee
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Mammalia;
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atggacgtggtcgacgagctggcgtacccgctggcgctgcgcggtcctcggcctgctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Sushiro-chou Tsurumi-ku, Tokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
Clones are derived from the chimpanzee BAC library PTB This BAC encars generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T. Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 41. 90; Conservative
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R.Site 2
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/clone_lib="PTB Chimpanzee Male
476 c 700 g 14 t 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-003A20.F"
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1. .1341
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Eutheria; Primates;
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GSS; GSS (genome survey
Pan troglodytes male ly
                                                                                                                                                                               AG060116 1278 bp DNA Pan troglodytes DNA, clone: PTB-047106.F, AG060116
and Chemical Research (RIKEN), (
1-7-22 Suehiro-chou, Tsurumi-ku,
                 Direct Submission Submitted (02-AUG-2001) Asao Fujiyama,
                                    Fujiyama, A., Hattori, M., To
Totoki, Y., Watanabe, H. and
                                                                Unpublished
                                                                                 Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y.
                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                   Pan troglodytes
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troglodytes male lymphoblast DNA,
Library clone:PTB-047I06.F.
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                                                                          end sequences of Library PTB
                                                                                                                Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Pan.
1) Asao Fujiyama, The Institute of Physical (RIKEN), Genomic Sciences Center (GSC); surumi-ku, Yokohama, Kanagawa 230-0045, Jap
                                     Toyoda, A., nd Sakaki, Y.
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                                              Taylor, T.D.,
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                                        cacgaccgcggcctgatgagtcgcaacgagatcgtcagcacggtggtcacgttcatcttc
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                                                                                                                                                                                                                                                                                                                                                                                                                             (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC enwas generated during the R&D process and may have higher chance of
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                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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Pan troglodytes male lymphocytes DNA,
Male BAC Library clone:RP43-040F09.TJ
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Totoki, Y., Watanabe, H. and
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Totoki, Y., Watanabe, H. and Sakaki, Y
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Pan troglodytes DNA, clone: RP43-040F09.
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/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC
/clone_lib="RFCI - 43 Chimpanzee Male BAC
/ 778 c 655 g 0 t 365 other
                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
/db_xref="taxon:9598"
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nd Sakaki, Y.
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BG852363 1024034A03.y2 Chlamydomonas

C. reinhardtii CC-1690, reinhardtii cDNA, mRNA s

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Contact: Charles Hauser
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Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation
Vascular Plants; project phase 2
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McDermott,J.P., Silflow,C., Stern,D. a
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1 (bases 1 to 1281)
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Durham, NC 27708-1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the EcoRI (5′) and XhoI (3′) sites. pBluescript II SK- plasmids were excised from the lambda ZAP clones by superinfection with Exassist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806."
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/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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COMMENT REFERENCE REFERENCE SOURCE KEYWORDS TITLE AUTHORS TITLE AUTHORS ORGANISM JOURNAL JOURNAL (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
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Tel:81-45-503-9110, Fax:81-45-503-9110, Fax:81-503-9110, Fax:81-503-9110, Fax:81-503-9110, Fax:81-503-9110, Fax:81-503-9110, Fax:81-503-9110, Fax:81-503-9110, Fax Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 330-0045, Japan Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D.,
Totoki,Y., Watanabe,H. and Sakaki,Y. GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB
BAC Library clone:PTB-016J15.F. Direct Submission Unpublished Fujiyama;A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y
BAC end sequences of Library PTB Mammalia; Eutheria; Eukaryota; AG039481.1 GI:16568206 (bases 1 to 1299) (sites troglodytes Metazoa; Chordata; Craniata; Vertebrata; Sutheria; Primates; Catarrhini; Hominidae; Taylor, T.D., Yada, Yada, T., Euteleostomi; Chimpanzee Male

clone tracking errors

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/db_mref="PTB-016J15.F"
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Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujiyama, A., Hattori, M., Toyoda, A., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
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Pan troglodytes male lymphoblast DNA, clone_lib:PTB
BAC Library clone:PTB-003A20.F.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Pan troglodytes DNA, clone: PTB-021P18.F, genomic su AG043615
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GSS; GSS (genome survey sequence).
Pan troglodytes male lymphoblast DNA, clone_lib:PTB
BAC Library clone:PTB-021P18.F.
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        Fujiyama,A., Hattori,M., To
Totoki,Y., Watanabe,H. and
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les 350; Conservative
gatgagtcgcaacgagatcgtcaggcacggtggtcacgttcatcttcaccggccacgagac 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbeségsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library PTB This BAC ence was generated during the R&D process and may have higher chance of
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Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
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/cell_type-"lymphoblast"
/clone_lib-"PTB Chimpanzee Male BAC Library"
/clone_lib-"STA g 34 t 206 others
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/db_xref="taxon:9598"
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Query Match 7.9%;
Best Local Similarity 44.3%;
Matches 396; Conservative
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Pan troglodytes DNA, clone: PAG043044
AG043044.1 GI:16571769
GSS; GSS (genome survey seque Pan troglodytes male lymphobl
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                                                                                                                                                                                                                                                                                                                                                  Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1134)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                Sequencing: M13Rev
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troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee
Library clone:PTB-021D20.R.
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                                                                                   Location/Qualifiers
                                                                                                                                                            /organism="Pan troglodytes"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                 : pKS145
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Score 95.6; DB 1
Pred. No. 0.0065;
0; Mismatches 48
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Search completed: June 21, 2002, 16:16:27 Job time: 6717 sec

Page 14

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BOWER, S. Grant., Perkins, J.B., Yocum, R. Rogers. and Pero, J.G. Biotin biosynthesis in bacillus subtilis
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1 (bases 1 to 10000)
Bower,S., Perkins,J.B., Yocum,R.R., Howi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cloning, sequencing, and characterization biotin biosynthetic operon
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USA,
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                                                                                                                                                                                                             gThrLeuAspArgGlyAlaSerAlaGluAspMetArgArgGlyHisAlaA 187
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                                                                                                             laIleAlaGluPheAlaAspTyrValGluArgAlaLeuAlaArgArgArg 203
                                                                                                                                                                 AACGATTGATTTTACCCGCTCAAGAAAGGCATTAACAGAGGGCAATATTA
                                                                                                                                                                                                                                                            CCGGAGGAAGATAGGGAGCAATTAAAGGAGTGGGCTGCGAGTCTCATTCA
                                                                                                                                                                                                                                                                                                       ProAlaAlaAspTrpGlyAlaValGlyArgTrpSerArgAspValGlyAr 170
                                                                                                                                                                                                                                                                                                                                                      ACTTTGCTTTTCCTTTAGCAAGTTTTGTCATAGCTAACATTATAGGTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGCGAGATTCAAAGTCCGCACCCCGCTGCCTGAGAGCTCAACCAAATA 7372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGACACATTGCGAGCTGTTCATCCTATCTATAAAGGGAGTTTCTTAAAAT 7272
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//protein_id="AAB17464.1"
//d_xreef="GI:1277032"
//d_xreef="GI:1277032"
//translation="Modinahsuknrledmliygellmealicvlpeihviaaseatve
EVVSKRFILIPTESLDAYRYIESTDIIYKSLLVSVEVTVIGTAVSMELSSLMAYGLS
RRDLIGRQPIMELVVETMLESGGMIPFEVVVKSIGLLDSYMALIPTAINAFMLIILK
NFFQNIPSSLEESAKIDGCNDLGIFFKIVLPLSLPALATISLFYAVTYMNTYMTAILY
LNDAAKMPIQVLLRQIVIVSSGMQGDMSEMGSGSSPPPEQTIG"
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ISM Bactlius Subtilis

Bacteria; Firmicutes; Bacillus/Clostridium group;

Bacteria; Firmicutes; Bacillus/Clostridium group;

Bacteria; Firmicutes; Bacillus/Clostridium group;

Bactlius/Staphylococcus group; Bacillus.

CE 1 (bases 1 to 215640)

RS Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Azevedo, V., Bertero, M.G., Bruschi, C.V., Caldwell, B., Capuano, V., Boro, S., Brouillet, S., Eruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entlan, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Gandi, G., Guiseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, K., Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P.,
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REFERENCE
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Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardinois, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mauel, C., Medigue, C., Medina, N., Mellado, R.P., Mizuno, M., Moestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Portetelle, B., Porwollik, S., Prescott, A.M., Presecan, E., Pujic, P., Purnelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadaie, Y., Sato, T., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadaie, Y., Sato, T., Scanlan, E., Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J., Sekowska, A., Seror, S.J., Serror, P., Shin, B.S., Soldo, B., Sorokin, A., Tacconi, E., Takagi, T., Takahashi, H., Takemaru, K., Takeuchi, M., Tamakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Viari, A., Wambutt, R., Wedler, E., Wedler, H., Weitzenegger, T., Winters, P., Wipat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, H. and Danchin, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur, Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724 Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45 68 89 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Danchin, A.

The complete genome sequence of the gram-positive bacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1020. .2270)
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/db_xref="SPTREMBL:034430"
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KASYFLYESAKRLLDSNEESKISD"
                                                                                                                                                                                                                                                                                                                                                      /product="hippurate hydrolase"
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/db_xref="GI:2635413"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(99. .1001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bacillus subtilis"
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DLGVGKAPGGFQLSTDALQAEYKKPVRQFDEKLEELTHFVRDDFPDTHRYAALRPRPQ
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                                                                                                                 /gene="hisP"
                                                                                                                                         complement(5649. .6428)
                                                                                                                                                            /gene="hisp"
                                                                                                                                                                                     complement (5649)
                                                                                                                                                                                                                           VDRKPGIFLLGGSTESAISAAKLGISFVFAYFINGEEEVLKEARRAFDAHLPPGSEAE
FHLAPAVFAAHTKEEAEKHIVSRESIKVVLKDGRKVNVGSREQAEAYLENVTEPYDII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4648. .5652)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4648. .5652)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSDVVNIVVWSKKGCSYCEEVKNYLNEKGFPFQNIDVSEKEKLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4352. .4633)
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/gene="ytnI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
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/gene="ytnJ"
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SYVEESEENILG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MTIIAGTVVKGKQLGRKLGFPTANVDAKIHGLRNGYYGVLATVNHQFHLGVMNIGVKPTVGSNLEKTLEIFLFDFHRDIYGEKIECSILFKIREERRFDSLESLTKQIKKDISCVAKRFELIGIMAPNKKESLLSHQELNLPDLCFYKKCNNLYGVNRGV
                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:034846"
                                                                                                                                                                                                                                                                                                                                                                                                                                           transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="ytm0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="CAB14910.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGTLDAFVEKVIPILQERGLYRQDYRGGTLRENLGLGIPQHQSVLHSSHH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTEEEAEKKYREFAELIPIENAVTYLARFFDDYDLSVYPLDEPFPDIGDVGKNAFQST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to nitrilotriacetate monooxygenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="transcriptional regulator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ribR"
/function="regulation of riboflavin biosynthesis genes"
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US-09-724-797-36 x BSUB0016/rev
91374 TCATTTGCTTGATCAAGTGCAAGGTAAAAAAAAAAGATGGAGGTCATTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91665 CGACACATTGCGAGCTGTTCATCCTATCTATAAAGGGAGTTTCTTAAAAT 91616
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                                                        paspLeuLeuArgProAlaLeuAlaArgGlyAlaMetAspValValAspG 137
                                                                                                                                                                                                                                         AGAACCAGCCTGATCATAGACGATTGCGGACGCTTGCCAGCGGAGCGTTT
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Henkin, T.M. Glass, B.L. and Grundy, F.J.
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regulatory sequence in multiple tRNA synthetase genes
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Grundy, F.J. and Henkin, T.M.
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Nucleotide sequence of the Bacillus subtilis phor
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Green, C.J., Stewart, G.C., Hollis, M.A.,
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
Kiel, J.A., Boels, J.M., Beldman, G. and Venema, G. Glycogen in Bacillus subtilis: molecular characterization operon encoding enzymes involved in glycogen biosynthesis
                                                                                                  11 (bases 162129 to 164080)
Grundy, F.J., Waters, D.A., Allen, S.H. and Henkin, T.A.
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                                                                                                                                                                                                                          Grundy, F.J., Waters, D.A., Takova Identification of genes involved acetoin in Bacillus subtilis
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96345628
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transcription factor sigma H

Mol. Microbiol. 20 (2), 339-350 (1996)
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Domaine de Vilvert, Jouy-en-Josas cedex 78352, France
Location/Qualifiers
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wer,S., Perkins,J.B., Yocum,R.R., Howitt,C.L.,
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    /organism="Bacillus subtilis"
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/product="tRNA-Met"
6531. .6607
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6079. .6151
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6251. .6327
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/product="trNA-Lys"
5629. 5715
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6172. .6248
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/product="tRNA-Leu"
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2203. 5129
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                                                 The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at http://www.nih.go.jp/
jun/ggi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hrMetPheArgGlyLeuAlaSerLeuProIleAlaPhe 398
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Streptomyces coelicolor cosmid H10.
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Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 39524)
Redenbach, M., Kleser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABC transporter; adenylosuccinate synthetase; aspartate aminotransferase; ATP-dependent protease ATP-binding subunit; cytochrome P-450 hydroxylase; fba; fructose 1,6-bisphosphate aldolase; lipase/esterase; oxidoreductase; pura; RNA polymerase sigma factor; spermidine synthase; transmembrane efflux protein; two-component regulator; two-component sensor kinase; uridine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL; http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (05-MAY-1999) Streptomyces coelicolor sequencing project, sammer Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 39524)
James, K.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinashi, H. and Hopwood, D.A.
A set of ordered cosmids and a detailed genetic and physical map
for the 8 mb Streptomyces coelicolor A3(2) chromosome
mol. microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL049754.1 GI:4753846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murphy, L. and Harris, D. Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by the BBSRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'-monophosphate synthase
                        upstream initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 39524)
sequence MAY NOT be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .GCGGATTTTGAATGGCGGTATCGGCCGCTTT 89846
   the entire
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   insert of
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for small overlap between neighbouring submissions.

Cosmid H10 lies between 6673 and H44 on the AseI-H genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restriction fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yenne="SCHIO.03c" //oene="SCHIO.03c" //oene="SCHIO.03c" //oene="SCHIO.03c" //oene="SCHIO.03c, hypothetical protein, len: 96 aa; unknown function, probable CDS suggested by positional base preference, GC frame analysis and amino acid composition"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SCH10.03c"
complement(1143. .1433)
/qene="complex"

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/note="SCH10.02, hypothetical protein, len: 221 aa;
/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
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/protexn_id="CAB42011.1"
/db_xref==07.01.4753848"
/translation="MRSPLLACDLWLVPLVDVLCHTPDNPFABELAQYDKVLAEAGLP
/translation="MRSPLLACDLWLVPLVDVLCHTPDNPFABELAQYDKVLAEAGLP
PVPVYQYMPGLAGEVAFVAGFDYDALHFLSSDELLAGGGGLVFTVDDELGGDYEQLLEM
FESTAQOSHLVWHYDHAGAYVPVDFDHPLSSDELLAGGGGLVFTVDDELEAVAFAL
FESTAQOSHLVWHYDHAGAYVPVDFDHPLSSDFLAGGGFUTSSSHTLLREELEAVAFAL
FESTAQOSHLVWHYDHAGAYVPVDFAPHDSSPFARERHVWLGLHAAATRSLAQGSMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462.
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FGNPYLCDFLHRLRVOSWVCTVQHLRRLSELRGALWSGHTALVDALARRDVPGARALV
DAYNGHSLALIEGLAGE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35101
complement(1472. .2356)
/gene="SCH10.04c"
/gene="SCH10.04c, probable RNA polymerase sigma factor,
/note="SCH10.04c, probable RNA polymerase sigma factor,
len: 294 aa; similar to many e.g. TR:005735 (EMBL:087308),
sigE, Mycobacterium avium extracytoplasmic function
                                                                                                                                                                                DGRRTALLVFDMQDSSQMPPIGEPFLMELNAEVDLCPIMNGDDLAKGLSQLG"
complement(1472. 2356)
/genpe-"SCH10.04c"
complement(1472. 2356)
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/protein_id="CAB42010.1"
/db_xref="GI:4753847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11/label=SCH10.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Streptomyces coelicolor A3(2)"
/Strain="A3(2)"
/db_xref="taxon:100226"
/clone="cosmid H10"
                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
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/db_xref="GI:4753849"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SCH10.01"
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/label=SCH10.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="SCH10.01"
                                                                                                                                                                                                                                                                                                                                                                     translation="MRVLLKATLDTEKSNEVIRSGRMEALIKETVDRIGPEAAYFGTI/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
/label=SCH10.03c
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                                                                                                                                                                                                                                 alignment_scores:
         alignment_block:
                                                                                                 Percent Similarity:
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/gene="SCH10.05c"
complement(2472. .2672)
/gene="SCH10.05c"
/note="sCH10.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 base preference, (composition" /codon_start=1 /transl_table=11 /label=SCH10.06c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     z-score:
overlap"
                                                                                                                                                           complement (3412. .4695)

/gene="SCH10.07c"
/gene="SCH10.07c"
/gene="SCH10.07c, purA, probable adenylosuccinate
/note="SCH10.07c, purA, probable adenylosuccinate
synthetase, len: 426 aa; similar to many e.g.
SW:PURA_ECOLI (EMBL:J04199), purA, Escherichia coli
adenylosuccinate synthetase (431 aa), fasta scores; op
1421 z-score: 1608.0 E(): 0, 50.5% identity in 420 aa
/overlap. Contains Pfam match to entry PF00709
                                                                                                                                                                                                                                                                                                                                                                             /gene="SCH10.07c"
/note="purA"
complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(2749...3240)
/gene="SCH10.06c"
/note="SCH10.06c, hypothetical protein, len: 163 aa;
/note="SCH10.06c, hypothetical protein, len: 163 aa;
unknown function, probable CDS suggested by positional
base preference, GC frame analysis and amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="SCH10.05c, hypothetical protein, l
unknown function, probable CDS suggested
base preference and GC frame analysis"
                                                   synthetase active site and PS01266 Adenylosuccinate synthetase GTP-binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRVRGVPAPEADLPRRRRAVDAYLAATRGGDFDALVALLHPDVVLSADAAVVPTPEPV
TVSGMEQVARGAMASMARARSAAVVLVDGMVGMAMAENGRLRVVLRFDFAADGRITGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mparsddmarqfeldrprlravayrilgslgeaddalqeawlra
drantsevgnpsgwlttvvarvclnllrardtrreeplddaarrqpaatgtaadpaee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alternative sigma factor (251 aa), fasta scores; opt: z-score: 266.2 E(): 1.6e-07, 29.8% identity in 168 aa
                                                                                                             Adenylsucc_synt, Adenylosuccinate synthetase, score 742.40, E-value 1.9e-219, PS00513 Adenylosuccinate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein"
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IVSRLPDDIPGASRDWALGDGVASWGGQKAVFRCGAEELQPNVNLCVTADGVDWVLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCH10.06c"
complement/77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="CAB42014.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DVIAEPARLNELDITGIG"
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/protein_id="CAB42013
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/transl_table=11
/label=SCH10.04c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARLKRDGVSVLRTYGRSPAVEFTYSGPREEVGGILTALDPAVKWIPQERKCIGLDDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GI:4753850"
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation-"MTDRYSAASCQGPYGGENGPEDCGDPYRFEVARHLRAPLRYCPY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=SCH10.05c
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                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al protein"
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d by p
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Quality: Ratio:

572.50 2.272 61.017

Percent

Identity: 33.656

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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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	CDS	CDS	gene CDS	CDS	CDS	
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                                                                                                                                                                                                               GlyLeuLeuGlyLeuProAlaAlaAspTrpGlyAlaValGlyArgTrpSe 165
|||||||||:::||| | ||||||
| GAACTGCTGGGAGTGCCCAAGGCGGACCAGGACGTGTTCCGCCAGTGGAC 155:
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SOURCE
ORGANISM
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asp...ValGluLeuArgGlyArgArgLeuArgArgAspAspValValVa 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysLeuArgTyrAspProSerValGlnSerAsnThrArgGlnLeuAspVal 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uAspLeuLeuArgArgArgProAspLeuLeuAlaGlnAlaValGluCluC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATCTGATCGGCAACGGCACCCTGGCCCTGCTGCGCCACCCCGACCAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerGlnValGlyAsnAlaValLeuSerLeuLeuAlaHisProAspGlnLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCGCTGATCGCGGCCCGGGACGACGACGACCGGCTGAACGAGGCCGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCGGAGCAGTTGCGATGGCAGCGGAGCCTCACGGTCCGAGGACTGGAA 16226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt laSerAspAlaLeuAlaTyrGlnProArgThrMetPheArgGlyLeuAla}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCGTTCCACGGACTGCTGCCCGGCCTGCCCGGCCTTGCGCTGTCCGTAC 16176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAACCCATCGAGGTGGCGGGCACGCGCATCGAGAAGGGCCCACCCGGTGCT
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Stover,C.K., Pham,X.Q., Erwin,A.L., Mizoguchi,S.D., Warrener,P., Hickey,M.J., Brinkman,F.S., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrock-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R., Smith,K., Spencer,D., Wong,G.K., Wu,Z. and Paulsen,I.T. Complete genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                                                                                                                                                                               ÃE004675 AE004091
AE004675.1 GI:9948522
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                               complement(3008. .4342)
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                                                                                                                                                                                                                                                                                                                                         complement(3008. .4342)
                                                                                                                                                                                                                                                                                                                                                                                                FLNAYHEYGARNRSEGSRLILRYSQVF"
                                                                                                                                                                                                                                                                                                                                                                                                                                             {	t ANYSVSLALDAHWRLGLSGYSLRQITDERVDGHDRPDSRERVDAIGPALMFGWGKSRL}
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AINPGSNHWSFNPHYALTWEFAEGWEASARLQYLLPGKNRDPAPPLADDYLQPGQAFH
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YLLTNWLPTLIGGTGFSLGEAATISAMFQLGGTLGALLLGSAMDRFDAHRVLSLAYVG
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/protein_id="AAG05863.1"
                                                 /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YAAANRGATPTASAHEAFLTVSQPAELDRQLAAAKAEGQWVLLDYYADWCVSCRIMEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLGLGIGMPLLLLVTVGSRFLPKPGPWMNLVKGVFGFLFLGTAWILLRPLLGEALWIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TWERLDDGQVQLRWQTAPGYYLYQKRLRFDGLDPALQPQLPPGESHSDEFFGESQVYR
QSLELTLPAAAAGQLRLGWQGCADAGLCYPPQSQALDLGGTGPAAAGTSGEVAEDQGL
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/gene="PA2478"
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/gene="PA2477"
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                                                                                                                                                                                                                                                                                                                                                                /gene="PA2479"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGEVDAGGFLAHWQATRERG"
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alignment_block:
US-09-724-797-36 x AE004675/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4034 GCAATTGCAACCG.....CTGGCGCGCTTCTACGACAACTTCATGCTGT 3991
                                                                                                                                                                                                                                                                                                        119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTGGCGCCGCCGCCCAGGGGGGGGCGCCAGCTGGTTCGGCCACCA 4035
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yArgThrLeuAspArgGlyAlaSerAlaGluAspMetArgArgGlyHisA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAACGACGCGCGCGCACACCCGCCTGCGCAGGCTGTTCGCTCCGGCC 3941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heGlnAspGluProAspHisGlyArgLeuArgGlyValValGlyProAla 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGGTCTGCCGCGACCAGGCCTCGATCTGGTGGATCAGTCGCTATGCCG 4135
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                                                                                               LeuProAlaAlaAspTrpGlyAlaValGlyArgTrpSerArgAspValGl 169
                                                                                                                                                    GGGATTTCGCCGAACCGCTGACGATCCGGGTGGCCGCCGAGCTGTTCGGC
                                                                                                                                                                                                 spGluLeuAlaTyrProLeuAlaLeuArgAlaValLeuGlyLeuLeuGly 152
                                                                                                                                                                                                                                                                                                        lAspAspLeuLeuArgProAlaLeuAlaArgGlyAlaMetAspValValA 136
                                                                                                                                                                                                                                                                                                                                                        TTCGGCCCCGACGCCGTGCGCCCCCTGGGAAGCGCGCATCGAGGTGCTGGT 3891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pLeuValGlyProGlyLeuLeuAlaGluIleValGlyAspIleIleLeuP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .....ArgThrGlyIleArgArg......PheTrpThrAs 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGTTTCGGCGTGCCTGCGCGACCGCCGTTTCTCCGCCGACCCCGCTCGC 4085
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63.636
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RFWRHGKSGGSGLGLAIVQAIVQRCQCRLDFDSRADGLRVTLEMPLRE*

3683 c 3401 g 1427 t
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VERSION
KEYWORDS
                                                                                                                                                                                                                                seq_documentation_block: LOCUS AF087022
                         REFERENCE
                                                                                                                                                                                                                                                                                       seq_name: gb_ba:AF087022
                                                                                                         SOURCE
                                                                                                                                                                                                           DEFINITION
                                                                                    ORGANISM
      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uArgAlaAlaValAlaAlaLeuAlaArgLeuProGlyLeuArgLeuGlyC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyAlaGlyMetArgTyrCysLeuGlySerTyrLeuAlaArgThrGlnLe 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGAGGAGGTGGAGATCGGCGGCCAGCGGATTCCGCCTGGAGAGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValAlaSerGlnValGlyAsnAlaValLeuSerLeuLeuAlaHisProAs
                                                                                                                                                                                                                                                                                                                                 ACCCTGGAGCGCTTGCCGATC 3044
                                                                                                                                                                                                                                                                                                                                                                       GlyLeuAlaSerLeuProIle 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ysAlaSerAspAla.....LeuAlaTyrGlnProArgThrMetPheArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGACCGCCTGCAGTTGCAGCGAGCGAACGCCAAGCAGCACGTGGCGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pGlnLeuAspLeuLeuArgArgArgProAspLeuLeuAlaGlnAlaValG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGCTGAGCTTCCTCGCGGCGAACCGCGACCCGGAGATGTTCGCCGCCC
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| ::: |||||||||||||||
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                                                                                                                                                                  Streptomyces venezuelae complete cds. AF087022
Actinomycetales; Streptomycineae;
1 (bases 1 to 1470)
Betlach,M.C., Kealey,J.T., Ashley,
                                                         Streptomyces venezuelae
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                         Streptomyces venezuelae.
                                                                                                                                               AF087022.1
                                                                                                                                               GI:3746883
                                                                                                                                                                                                           cytochrome
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  Ashley, G.W.
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                                            Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                         P450 monooxygenase
    and McDaniel, R
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                                                                                                                                                                                                           (pick) gene,
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alignment_block:
US-09-724-797-36 x AF087022
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Quality:
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AUTHORS
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ORIGIN
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Percent Similarity:
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423 CCCGGCTGCGCAAGCTGGTGGCCCGTGAGTTCACCATGCGCCGGGTCGAG 472
                                                                                          338 GAC.....TGGCGCAACTCCACGACTCCCCTGACCGAGGC 372
                                                                                                                                                                                                                                                                                                       288
                                                                                                                                                                                                                                                                                                                                                                                            238 TCCGGCCCACCGGGTGCGCACCCCCGAGGGGGACGAGGTGTGGCTGGTCG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188 GATTTCGCGGCCGATCCGTATCCGACGTACGCGAGACTGCGTGCCGAGGG
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                         93 lyArgLeuArgGlyValValGlyProAlaPheSerProSerAlaLeuArg 109
                                                                                                                                                   77
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                                                                                                                                                                                                                                                                                                                                                                                                                                   31 pProValHisArg...........GlyAlaHisArgValTrpTyrValS 44
                                                                                                                                                                                                                                           61 ThrGlyIleArgArgPheTrpThrAspLeuValGlyProGlyLeuLeuAl 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 AspValArgArgAspProTyrProSerTyrHisTrpLeuLeuArgHisAs
                                                                                                                                                                                                                                                                                               TCGGCTACGACCGGGCGGGCGGTCCTCGCCGATCCCCGGTTCAGCAAG
                                                                                                                                              aGlu...IleValGlyAspIleIleLeuPheGlnAspGluProAspHisG 93
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McDaniel,R. and Betlach,M.C.
Direct Submission
Submitted (25-AUG-1998) Kosan Biosciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burlingame,
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PMIRGLKALPIRWRRGREAGRRTG"
3 559 c 480 g 223 t
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2.216
61.055
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/strain="ATCC15439"
/db_xref="ATCC:15439"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="synthesis of picromycin, methymycin, and
neomethymycin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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	etPheArgGlyLeuAlaSerLeuProIleAlaPheThrProGly 401 ::: ::: ::: FATCCGCGGGCTCAAGGCCCTGCCGATCCGCTGGCGGCGAGGA 1345	387 1302
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272 951	AspLeuLeuAl ACGCTCTTGGA	256 902
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126 522	ArgLeuGluProValIleAlaGlyThrValAspAspLeuLeuArgProAl	110 473

seq_name: gb_ba:AF079139

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DEFINITION
ACCESSION
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AUTHORS
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SOURCE
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LOCUS AF079139
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Direct Submilssion
Submitted (17-JUL-1998) Department of Microbiology, University,
420 Delaware Street SE 1060, P.O. Box 196, Minneapolis, MN 55455,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 4342)
Xue,Y., Wilson,D., Zhao,L., Liu,Hw. and Sherman,D.H.
Hydroxylation of macrolactones YC-17 and narbomycin is mediated
the pikC-encoded cytochrome P450 in Streptomyces venezuelae
Chem. Biol. 5 (11), 661-667 (1998)
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Streptomyces venezuelae
Streptomyces venezuelae
Bacteria; Firmicutes; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces venezuelae pikCD operon, complete sequence AF079139
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A gene cluster for macrolide antibiotic biosynthesis in
streptomyces venezuelae: architecture of metabolic diversity
Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12111-12116 (1998)
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                                                                                                                                                                                                                                                                                                                     RTSDEDGSRLTSEELLGMAHILLVAGHETTVNLIANGMYALLSHPDQLAALRADMTLL
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LGVPEPDRAAFRVWTDAFVFPDDPAQAQTAMAEMSGYLSRLIDSKRGQDGEDLLSALV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene='
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibiotics methymycin,
                                                                /product="putative transcriptional activator
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/db_xref="GI:3800841"
                                                                                                                                                                                                                        /gene='
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organ1sm="Streptomyces venezuelae"
/Strain="ATCC:15439"
/db_xref="ATCC:15439"
/db_xref="taxon:54571"
                                                                                                                                                                                                                                                                                                 PMIRGLKALPIRWRRGREAGRRTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"involved in the biosynthesis of macrolide antibiotics methymycin, neomethymycin, and pikrom
{	t NLTSPADAPLRVDETHRLHDWLLSVSRRTPFLVAVDDLTHADTASLRFLLYCAAHHDQ}
                    /translation="MNLVERDGEIAHLRAVLDASAAGDGTLLLVSGPAGSGKTELLRS
LRRLAAERETPVWSVRALPGDRDIPLGVLCQLLRSAEQHGADTSAVRDLLDAASRRAG
                                                                                                                                                /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="catalyzes the hydroxylation of YC-17 into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="pikC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="pikCD operon"
                                                                                                                                                                                                 /gene="pikD"
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RAPAYHATTGGNUFLLRALTQDRQASHTTLGAAGGDEPVHGDAFAQAVLOCLHRSAEG
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PSHPVMALIRCLYWYGRLPEAADALSRLRPSSDNDALELSLTRWMLAALCPPLLESL
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RAELALSHAAPESWGLAVGMPLSALLAEAVERRSLGWEAVFATRAMIAIRGGDLFTARE
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ALAGMSRHQQAQGDNYRAEMTARLAGDMAWACGAYFLAEEIVPGRGGRRAKAVSTELE
LPGGFDVGLLSBAERRVAALAARGLTNRQIARRLCVTASTVEQHLTRVYRKLNVTRRA
DLPISLAQDKSVTA"
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alignment_block:
US-09-724-797-36 x AF079139
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                                                                                                                                  CGCGCCGCCTTCCGCGTCTGGACC....
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heAlaAspTyrValGluArgAlaLeuAlaArgArgArgArgGluGlyGly
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                                                CTTCGTCTTCCCGGACGATCCCGCCCAGGCCCAGACCGCCATGGCCGAGA
                                                                                    gGlyAlaSerAlaGluAspMetArgArgGlyHisAlaAlaIleAlaGluP 191
                                                                                                                                                                                                                     CGCTGCCGATCACCGTGATCTCCGAACTCCTCGGCGTGCCCGAGCCGGAC
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DEFINITION
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                          FEATURES
                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                               JOURNAL
MEDLINE
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                                                                                                                         TITLE
                                                                                                                                                 AUTHORS
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                                             Andersen, J.F. and Hutchinson, C.R. Characterization of Saccharopolyspora erythraea cytochrome P-450 genes and enzymes, including 6-deoxyerythronolide B hydroxylase J. Bacteriol. 174, 725-735 (1992) 92121109
                                                                                                                                                                                                                                      cytochrome P450.
Saccharopolyspora erythraea (library: NRRL 2338)
Saccharopolyspora erythraea
Bacteria; Firmicutes; Actinobacteria; Actinobacte
                                                                                                                                                                                                                                                                                                                                                                                        SERCP450A 3078 bp DNA linear E Saccharopolyspora erythraea ORF 1 gene, partial cds.
                                                                                                                                                                       Saccharopolyspora
1 (bases 1 to 30)
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Ratio:
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.IleArgArgPheTrpThrAspLeuVal...GlyProGlyL
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SLAATISFADERTSAALADARLAFTQAQSATMTAGLACALAGAAVAMLSLRSGRASA
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RLRKLYVKAFTARRVEGLRPRIEQITDDLLDRLAGRSEVDLIDEFAFPLPITVISELM
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AVEDGDRLSEGELIAMVFLLLVAGHETTVNLIGKCVLSLLGNPDQLAALKNDPSLLPG
ALEETLRYESPVANGTFRHTAEAVRFGDVVIPEGELVAVVALGAANRDGERFEDPDRFD
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1 1060 c 1137 g
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/codon_start=1
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ARGHHQHLRLRRGAGGHLGGRDRPGNQPRVRDQGAGEQGGPVAGRRAQAHLAGALGHG
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                                                                                                                    AspProValProSerMetSerPheGlyAlaGlyMetArgTyrCysLeuGl 350
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TITLE
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ORGANISM
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Wheeler,P.R., Honore,N., Ganier,T., Churcher,C., Harris,D.,
Mungall,K., Basham,D., Brown,D., Chillingworth,T., Connor,R.,
Davies,R.M., Devlin,K., Duthoy,S., Feltwell,T., Fraser,A.,
Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Lacroix,C.,
Maclean,J., Moule,S., Murphy,L., Oliver, Quail,M.A.,
Rajandream,M.-A., Rutherford,K.M., Rutter,S., Seeger,K., Sime,
Simmonds,M., Skelton,J., Squares,R., Squares,S., Stevens,K.,
Taylor,K., Whitehead,S., Woodward,J.R. and Barrell,B.G.
Massive gene decay in the leprosy bacillus
Nature 409 (6823), 1007-1011 (2001)
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Mycobacterium leprae strain TN c
AL583924 AL450380
AL583924.1 GI:13093618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-FEB-2001) Submitted on behalf of the Mycobacterium leprae sequencing teams. The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 18A, UK Unitie de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Rouux, 75724, Paris Cedex, France. E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 342300)
Parkhill, J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 342300)
Cole, S.T., Eiglmeier, K.,
Wheeler, P.R., Honore, N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Details of M. leprae sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                           datbase containing the M. leprae sequences is available http://genolist.pasteur.fr/Leproma/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Notes
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                                                                                                                                                                                                                                                                         /gene="ML1963"
275. .430
                                                                                                                                                                                                              /note="Possible pseudogene of M. Rv3463 (Best blastx score 121)"
                                                                                                      /product="probable 483, .1484
                                                                                                                                                                                                                                                                                                                                                           /organism="Mycobacterium
/strain="TN"
                                                                                                                                                                                                                                                                                                                                                                                                         1. .342300
/gene="rmlB"
/note="Similar
                                  /note="ML1964"
183. .1484
                                                                              /gene="
                                                                                                                                                                                                                                                     /gene="ML1963"
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misc_feature 2:	P. NAS	アナア	He N	(DS		di di		misc feature 1	: 5	*>>	, , , , ,	<u> </u>	0.0	ag 02. U	· > >	CDS 1	// 5/ 1.		~ ~ .	misc_feature 49	ב. ס	71 RJ	SI /	<u>``</u>	<i>" > "</i>	S e	er y	S)	aı 78	a:
21692201 /gene="lpqH"	/protein_id="0AC39921.1" /db_xref="G1:13093621" /tanslation="MRHKLIAAIYAVTIMAGAAGCSGGTQAPTPSVSKTTNSSPTTVA /translation="MRHKLIAAIYAVTIMAGAAGCSGGTQAPTPSVSKTTNSSPTTVA SSIPDAAAGETKVTIGGQPQKVSGPVVCSTTNGKFSIAIGDMITGVIVGLEPDASVVH MAGLGTIDGVVIAFTBGVPSENANATKNGNTYQITGTASGVDNTGQQIHKSFEIEVTC R"	<pre>'codon_start=1 'transl_table=11 'product="possible lipoprotein"</pre>	lpqH Rv3763. Contains a sequence and a PS00013 sin lipid attachment sit	/gene="logH" /gene="logH" /mote="Similar to M. tuberculosis 19 kDa lipoprotein	/gene="log" /gene="log" /gene="ktl966"	dTDP-4-dehydrorhamnose 3,5-epimerase, score 308.80, E-value 6.5e-89"	="rmlC" ="Pfam match to entry	INISHKRITI I 1555LAHGE LALIJUNSY WYLICSAEY NY AKEHATCATUPULALUWP VV DGVDTHLSKRDATAPNLDDIRASGLLPTWDETQNE IANLGSK." 1492. 2025	/T-anslation="MNYSELDISGAWEITPTIHSDSRGMFFEWLTASRFSAFTGHRLD /Translation="MNYSELDISGAWEYTCYTGSVEDVYVDIRLGSPTFGCWTSIT	product="q")b-4-qenydrornamnose 3,5-epimerase" protein_id="CAC30920.1" db yrsf="g:-13093620"	transl_table=11	#PD sucar (see Ambold-services) (200 at 1): 0, 45.0% locality in 93 as overlap. Contains Pfam match to entry PF00908	TDD-4-dehydrorhamnose 3,5-epimerase SW:STRM_STRGR	3,5-epimerase rmiC Rv3465 TR:006330 (BMBL:295390) (202 aa); Fasta score E(): 0, 75.48 identity in 199 aa overlap, and to many others e.g. Streptomyces grisens	note="Similar to M. tuberculosis dTDP-4-dehydrorhamnose	1486 2094 /gene="rml C"	/yene="rmlC" /pote="rmlC"	-137"	note="Pfam match to entry PF01370 Epimerase, NAD	/gene="rmlB"	DDHNSAVWQILEKGQIGRTYLIGAENGHNNLTVLRTLLQMMGRDPNDFDHVTDRVGHD LRYAIDPTPLYNELCWAPKHANFDEGLRATIDWYRNNESWWRPLKDAVEARYEERGR"	FTILEAVRHHSVELHHISTDEVYGDLELDEPTRFTESTPYNPSSPYSATKAAGDMLV AMVRSYGYRATISNCSNNYGPYOHVEKFIPROTINVLTGRRPKLYGTGVNVRDWHY	TX3nSlation="MTMRLLVTGGAGFIGANFVHNAVRDHPDDTVTVLDAMTYAGRHE	protein_id="CAC30919.1" db_xref="GI:13093619"	/trans1_table=11 /product="dTDP-glucose 4,6-dehydratase"	pilletrase/Genyoracase ramily. Similar to Mi0204, ML0751, ML1942 and ML2428" Godon start=1	nty9% identity in 334 aa overlap. Contains Pram match to nty901370 Epimerase, NAD dependent	treptococcus pneumoniae DTDP-glucose-4,6-dehydratase cpsN R:054611 (EMBL:AF030364) (349 aa); Fasta score E(): 0,	and TR:Q50556 (EMBL:U43540) (329 aa); Fasta score E(): 0, 78.2% identity in 331 aa overlap, and to others e.g.	,6-dehydratase rmlB Rv3464 TR:O06329 (EMBL:Z95390) (331 a)
alignment_scores: Quality:	CDS	gene	repeat_region			CDS	gene	stem_loop				CDS	9 9	gene				CLO			repeat_region			CDS	gene			CDS	gene	
/: 521.00 Length: 400		<pre>/note="146 bp sequence found at 5'-end of copies 6 and 7 of LEPREP" complement(84618691)</pre>	/pseudo /transl_table=11 complement(80448189)	cumeracters remisposase in 2444-4 (smb4507) (500 da) fasta scores: E(): 0.00026, 41.3% id in 46 aa" (codon start=1		complement(75597698) /gene="Mil971" /gene="Mil971" /gene="Mil971" /gene="Mil971"	complement (75597698) /gene="ML1971"	protein" complement(66746727) /dene="Mr.1970"	/Fransi_table=11 /fransi_table=11 /product="putative group II intron maturase-related	ld in 216 aa" /codon_start=1 /nseudo	(Chesnut blight fungus) putative maturase TR.AAF27856 (EMBL:AF218567) (778 aa) fasta scores: E(): 7.8e-11, 29.2%	Complement(6211/334) /gene="MIL1970" /gene="MIL1970" /gene="MIL1970"		/pseudo /transl_table=11 complement(6211, .7354)	/codon_start=1	transposase tnpal TR:Q9R9U9 (EMBL:AJ245436) (355 aa) fasta	TR:Q44454 (EMBL:Z18270) (366 aa) fasta scores: E(): 0.0002. 51 5% id in 33 aa. and to Pseudomonas putida	בריים אל היים בריים ב	/gene="ML1969" /gene="ML1969"	<pre>/note="Dispersed repeat, LEPREP, copy 6" complement(58485946)</pre>	<pre>/product="PE family protein (pseudogene)" complement(5661, .8043)</pre>	/pseudo /pseudo /rans1 table=11	<pre>//note="Possible pseudogene of M. tuberculosis paralog PE" /nodon start=1</pre>	complement(54645649) /gene="ML1968"	645649)	/pseudo /trans_table=11 /product="ppp family protein (pseudogene)"	/note="Possible pseudogene of M. tuberculosis paralog PPE" /codon_start=1 /count_	.4995)	complement(47684995) /gene="ML1967"	<pre>/note="PS00013 Prokaryotic membrane lipoprotein lipid attachment site"</pre>

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alignment_block:
US-09-724-797-36 x MLEPRTN8/rev
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uArgArgArgProAspLeuLeuAlaGlnAlaValGluGluCysLeuArgT
                                                                                          GlyAsnAlaValLeuSerLeuLeuAlaHisProAspGlnLeuAspLeuLe
                                                                                                                                        CGTGCGGTCTGCTCGTTGCTGGTCATGAGACCACGGTGAATCTGATT
                                                                                                                                                                    hrValValThrPheIlePheThrGlyHisGluThrValAlaSerGlnVal
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                                                                                                                                                                                                                                                                                   uAspAlaHisAspArgGly...LeuMetSerArgAsnGluIleValSerT
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Streptomyces coelicolor sequencing with BSRC and Beowulf Genomics by the BBSRC and Beowulf Genomics by the BBSRC and Beowulf Genomics

Details of S. coelicolor sequencing at the Sanger Centre are available on the World Wide Web.

(URL: http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1.01c. SC (S. numbered using the following system eg SC7B1
                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (19-SEP-2000) Streptomyces coelicolor sequencing proj
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
Colney, Norwich, Norfolk NR4 7UH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J., Kinashi, H. and Hopwood, D.A.

A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome

Mol. Microbiol. 21 (1), 77-96 (1996)
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Streptomyces coelicolor
Streptomyces coelicolor
Streptomyces coelicolor
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Streptomyces.
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Streptomyces coelicolor cosmid E41.
AL442120
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ABC transport system ATP-binding protein; ABC transport system integral membrane protein; cytochrome P450 hydroxylase; eno, enolase; hydrolase; integral membrane protein; lipoprotein; nucleotidyltransferase; oxidoreductase; pkaE; secreted protein sensor kinase; transcriptional-repair coupling factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Streptomycineae; Streptomycetaceae; 1 (bases 1 to 36028)
Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saunders, D.C. and Harris, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 36028)
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Cambridge
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FEATURES
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jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-131p before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid E41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The lengt in codons is given for each CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(<1..951)
//gene="SCE41.01c"
//gene="SCE41.01c"
//note="SCE41.01c, probable oxidoreductase (fragment), len:
//note="ScE41.01c, probable oxidoreductase"
complement(1477. .2418)
/gene="SCE41.02c"
/gene="SCE41.02c"
/note="SCE41.02c, possible hydrolase, len: 313 aa; similar
to N-terminal region of SW:GPPA_ECOLI (EMBL:M87049)
Escherichia coli guanosine-5'-triphosphate,3'-diphosphate
pyrophosphatase (EC 3.6.1.40) GppA, 494 aa; fasta scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative oxidoreductase (fragment)"
/protetn_id="CAC09533.1"
/protetn_id="CAC09533.1"
/db_xref=="Ci:10741775"
/translation="MRYGEATVTVVDPRSYMTVQPELPEAAAGSISPRHVVVPLRRVL
/KRAFULTGRWTTIDQDRKVATVAPLYGEAYELPFDLLVTAMGAVSRTTPF1PGLAEQGI
GMKGIEESIGLRHNLLEDLDKADSTTDEEIRKALTFVFVGGGFAGAETIGEVEDMAR
DAAKYYNNVSREDMRFILVDAADKILDEVGPKLGQYGKEHLEGRGVEYYLSTSMDSCV
DGHVYLKNGLEVDSNTIVWTAGVKPNPALARFGLPLGPRGHDTQATLQVQGTDYIMA
                                                                                                                                                                                                                                                         complement(1477. .2418)
/gene="SCE41.02c"
                                                                                                                                                                                                                                                                                                                                            /note="Pfam match to entry PF00070 pyr_redox, Pyridine nucleotide-disulphide oxidoreductase, score 76.80, E-value 6.7e-22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(112. .798)
/gene="SCE41.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="nominal overlap with Streptomyces coelicolor cosmid SCE25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:100226"
/clone="cosmid E41"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1. .951)
/gene="SCE41.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain-"A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Streptomyces coelicolor A3(2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGDNAQVPDLVGRKAGNENAWCPPNAQHALRQAKVLGDNVI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11/
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/db_xref="taxon:1902"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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CDS

DIQEFMIAPIGAESFSEALRWGAEVYHTLKKVLKNKGLATGLGDEGGFAPNLGSNREA

JDLILEAIKEAGYTPGEQIALALDVAASEFYKDGSYAFEGKNRSAAEMTEYYAELVE!

gene

```
/notee_SCE41.05c, eno, enolase, len: 426 aa; similar SW:ENO_ECOLI (EMBL:X82400) Escherichia coli enolase (4.2.1.11) Eno, 431 aa; fasta scores: opt: 1603 z-scor 1807.6 E(): 0; 60.6% identity in 419 aa overlap. Cont Pfam match to entry PF00113 enolase, Enol-ase and match to entry PF00113 enolase, Enol-ase and match to entry PF00113 enolase, Enol-ase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3061..3585)

/gene="SCE41.04c"
/gene="SCE41.04c"
/note="SCE41.04c, hypothetical protein, len: 174 aa;
similar to TR:p96376 (EMBL:Z92539) Mycobacterium
tuberculosis hypothetical 24.6 kDa protein MrC10G2.25c,
228 aa; fasta scores: opt: 273 z-score: 32.6 E();
5.1e-11; 35.6% identity in 149 aa overlap. Contains
possible coiled-coil region at approx residues 87..106
/translation="MPSIDVVVAREILDSRGNPTVEVEVGLDDGSTGRAAVPSGASTG
AFEAIELROGDPSRYLGKGVEKAVLAVIEQIGPELVGYDATEQRLIDQAMFDLDATDN
KGSLGANAILGVSLAVAHAASEASDLPLFRYLGGPNAHLLPVPMMNILMGGSHADSNV
                                                                                                                                                                                                   /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                    Prosite entry PS00164 Enolase signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(3639. .4919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(3639. .4919)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MCGDVRACTGGGDQMAVKDRDRESTATRIRIIGEQTAARVYRSQ
TKRQARRSRLTGRAALLAMVLCSLVVALAYPIRQYVAQRAEIADLQREQRETRQRVED
LRDLKARWQDDAYAEQQVRLRUHYVMPGETGFVVVDPEAAEQTRARAGAADRPWYQNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SCE41.03c"
complement(3061. .3585)
/gene="SCE41.04c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2415. .2975)

/gene="SCE41.03c"
/note="SCE41.03c, conserved hypothetical protein, len: 1:
aa; similar to TR:P96375 (EMBL:292539) Mycobacterium
tuberculosis hypothetical 16.6 kDa protein MTCY10G2.24c,
155 aa; fasta scores: opt: 632 z-score: 730.7 E(): 0;
67.6% identity in 136 aa overlap"
                                                                                                            /protein_id="CAC09537.1"
/db_xref="GI:10241779"
                                                                                                                                                                     /product="enolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WDGVDKADAVARRQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
/protein_id="CAC09536.1"
/db_xref="GI:10241778"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="eno"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="SCE41.05c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="eno"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mQTPPPTTPRTEPTDADVAAFKQQLGRPPRGLRAIAHRCPCGQP
DVVETAPRLPDGTPFPTLYYLTCPKAASAIGTLEANGVMKEMTERLATDPELAAAYRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WWRKGPCVTPTEQTDETDETGQEDAQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AHEDYIRRRDEIEELTGFPSAGGMPDRVKCLHVLVAHSLAAGPGVNPLGDEAIAMLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="conserved hypothetical protein"
/protein_id="CAC09535.1"
/db_xref="GI:10241777"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(2415.
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/protein_id="CAC09534.1"
/db_xref="GI:10241776"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        opt: 311 z-score:
310 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at approx residues 87. .106"
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alignment_block:
US-09-724-797-36 x SCE41/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACGACGAGCCCGCGCACGCCAAGGGCAAGACCGGCATC.....
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                                  luAspMetArg.....ArgGlyHisAlaAlaIleAlaGluPheAlaAsp 193
                                                                                                                                                                                                                                                                                  spValValAspGluLeuAlaTyrProLeuAlaLeuArgAlaValLeuGly 149
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GGTCGGTGAAGAAGATGCGCGGCTAC......
                                                                               CATGATGATCCGTCACCAAGGGGGT.....CCGCGCGGCGGCGTAGCCC
                                                                                                                                                                                      LeuLeuGlyLeuProAlaAlaAspTrpGlyAlaValGlyArgTrpSer..
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                                                                                                                     .....ArgAspValGlyArgThrLeuAspArgGlyAlaSerAlaG
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complement(4926. .4931)
complement(5181. .5915)
/gene-"SCE41.06c"
complement(5181. .5915)
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seq_documentation_block:
LOCUS AL646080
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                                     REFERENCE
                                                                                                                 SOURCE
                                                                                                                               KEYWORDS
                                                                                                                                                                                                            DEFINITION
                                                                                                                                                  VERSION
                                                                                                                                                                    ACCESSION
                   AUTHORS
                                                                                           ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ProArgThrMetPheArgGlyLeuAlaSerLeuProIleAlaPheThrPr 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCTGCCGGACCTCCGCCTCGCCGGCCGACCCCGAACTCCGGTGGCGC
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                                                                                                                                                                                                                                                                                                                                                               400
                                                                                                                                                                                Ralstonia solanacearum GMI1000 megaplasmid, segment 5/11.
1 (bases 1 to 190050)
Salanoubat,M., Genin,S., Artiguenave,F., Gouzy,J., Mangenot,S.,
Arlat,M., Billault,A., Brottier,P., Camus,J.C., Cattolico,L.,
                                                                                             Ralstonia solanacearum.
Ralstonia solanacearum
                                                                                                                                                  AL646080 AL646053
AL646080.1 GI:17431113
                                                         Ralstonia.
                                                                           Bacteria; Proteobacteria;
                                                                               beta subdivision; Ralstonia
                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                  complete sequence;
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                                                                               group;
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JOURNAL
REFERENCE
AUTHORS
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Submitted (05-DEC-2001) Genoscope and CNRS UMR-8030, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biologie Moleculaire des Interactions Plantes-Microorganismes INRA-CNRS, BP27, 31326 Castanet-Tolosan Cedex, France, Fondation Jean Dausset-CEPH, 27 rue Juliette Dodu, 75010 Paris, France, LMGM CNRS 118 Route de Narbonne, F 31062 Toulouse Cedex 4, Genoscope and INRA URGY, 2 rue Gaston Cremieux, CP5706, 91057 Evry Cedex, France, Laboratoire de Biometrie et Intelligence Artificielle INRA, BP27, F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire Christian Boucher@toulouse.ins.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chandler,M., Choisne,N., Claudel-Renard,C., Cunnac,S., Demange,N., Gaspin,C., Lavie,M., Moisan,A., Robert,C., Saurin,W., Schiex,T., Siguier,P., Thebault,P., Whalen,M., Wincker,P., Levy,M., Weissenbach,J. and Boucher,C.A.

Genome sequence of the plant pathogen Ralstonia solanacearum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
2 (bases 1
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/note="Product confidence: probable
Gene name confidence: hypothetical
predicted by Codon_usage
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Gene name confidence; hypothetical
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predicted by FrameD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted by Codon_usage predicted by FrameD"
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/note-"Product confidence : probable
Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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Gene name confidence :
                                                                                                                                                                                                                                                                                                                  PAREARQWLQATLDAMATHSPTMLHYTREALLRGRQLTLAECFRMELGIVARAIEEGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2336.
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1244. .2260
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                                                                                                                                                                                                                                                                                                                                                                                   agdpgdlmqalrrvfeppcnivphaaiarttpwivryfdrrstidrivatlreslerd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAIRLCARQEGMLTDPVYEGKSMHGMIDRVRGGEFPEGSRVLYAHLGGVPALNAYSFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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'FrameD"
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hypothetical
                                                                                           degradation; carbon
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alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-724-797-36 x AL646080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AL646080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                 77477 CATCGGGCCGAATGCGTTGATGACGGGGCACTACAGCATCGTCGACGCCC 77526
                                                              77624 CCGGATGTTCCTGATGCTCAATCCGCCCATGCACACGCGCCTGCGCGCCC 77673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77427 AATCCCTATCCCCTGTACGAGACGCTTCGCTCGCAGGGCCCCCTTCGTGCG 77476
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                                                                                                                                                                                                                                                                                                                                              52 alleuGlyAspGluArgPheAlaArgThr.....GlyIleArgArg 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 gGlyAlaHisArgValTrpTyrValSerArgPheAlaAspValArgAlaV 52
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                                                                                                                                                                                                         PheTrpThrAspLeuValGlyProGlyLeu...LeuAlaGluIleValGl 81 ::: ||| || ||| ::: ::
                                                                                                          yAspIleIleLeuPheGlnAspGluProAspHisGlyArgLeuArgGlyV 98
                                                                                                                                                                                                                                                                                      TGCTGCACAACCGGCAGATGGGCAAGAGCTACATGGAGAGCATCCGCCTG 77576
                                                                                                                                                                           CGATACGGCGAC...GAAGGCCCCAACATGCCGCTGTTCCAGGGGTTCAG
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1.952
67.442
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Gene name confidence: putative
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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predicted by Homology
predicted by FrameD*
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function="small molecule metabolism;
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	rolleAlaPhe 398	395
395 78570	pAlaLeuAlaTyrGlnProArgThrMetPheArgGlyLeuAlaSerLeuP	378 78521
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77723	TGATGATGCAGGTGTTCAACGCGCGGCAGATCGAATCGA	77674

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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Quality:
Ratio:
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US-09-724-797-36 x A60304
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TITLE
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                                                            87 lnaspGluProAspHisGlyArgLeuArgGlyValValGlyProAlaPhe 103
                                                                                                                                                                                                                                                                                                                                                                                                441 CCCTACCCGGTCTACCGGCGCTACCGGGAGGCCGCCCCGGTCCATCGCAC 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_RNA
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               104 SerProSerAlaLeuArgArgLeuGluProVallleAlaGlyThrValAs 120
                                                                                                                             585 CGCGTGGCCTCCGGCGACACCGGCCCGACACCGCGCCCGTCCCGATCCC 634
                                                                                                                                                                                                                                                                                                                               491 GGCGGCGGGCCCCGGAAAGCCTGACACCTACTACGTGTTCACCTACGACG 540
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                                                                                                                                                                                                                           65 ArgPheTrpThrAspLeuValGlyProGly.....
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                                                                                                                                                                                                                                                                                                                                                             36 .....GlyAlaHisArgValTrpTyrValSerArgPheAlaA 48
                                                                                                                                                                                                                                                                                                                                                                                                                .....LeuLeuAlaGluIleValGlyAspIleIleLeuPheG 87
TCACCCTCGATCGTCACCGGCCTGCGCCCCCCGCATCGCCGAACTCGCGAG 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unidentified.
unidentified
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1 (bases 1 to 6085)
1 Chases 1 to 6085)
1 Schupp, T., Engel, N., Bietenhader, J., Toupet, C. and Pospiech, A. STAUROSPORIN BIOSYNTHESIS GENE CLUSTERS
PAtent: WO 9708323-A 4 06-MAR-1997;
CIBA GEIGY AG (CH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4 from Patent WO9708323.
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5071. .6085
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1. .6085
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/db_xref="taxon:32644"
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593, .4011
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Percent Identity: 36.364
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366 1523	GlySerTyrLeuAlaArgThrGlnLeuArgAlaAlaValAlaAlaLeuAl	350 1476
349 1475	rgAspProValProSerMetSerPheGlyAlaGlyMetArgTyrCysLeu	333 1426
333 1425	aAsnArgAspProArgArgTyrAspArgProAspAspPheAspIleGlua	316 1376
316 1375	GlyArgArgLeuArgArgAspAspValValValValLeuAlaGlyAlaAl::::	300 1326
299 1325	roSerValGlnSerAsnThrArgGlnLeuAspValAspValGluLeuArg	283 1276
283 1275	gArgProAspLeuLeuAlaGlnAlaValGluGluCysLeuArgTyrAspP ::: CACACCGGAGTCGACACCGGCGGCGGCGTCGAAGAGCTGATGCGGTAACGACC	266 1226
266 1225	AlaValLeuSerLeuLeuAlaHisProAspGlnLeuAspLeuLeuArgAr 	250 1176
249 1175	alThrPheIlePheThrGlyHisGluThrValalaSerGlnValGlyAsn	233 1126
233 1125	aHisAspArgGlyLeuMetSerArgAsnGluIleValSerThrValV :::	217 1076
217 1075	ArgArgArgAluGlyGlyAspLeuLeuAlaLeuMetLeuAspAl 	201 1026
200 1025	lyHisAlaAlaIleAlaGluPheAlaAspTyrValGluArgAlaLeuAla ::::: ::: :::	184 976
184 975	pValGlyArgThrLeuAspArgGlyAlaSerAlaGluAspMetArgArgG:::::	167 935
167 934	.ProAlaAlaAspTrpGlyAlaValGlyArgTrpSerArgAs	154 885
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BASE COUNT
ORIGIN
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AUTHORS
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FEATURES
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LOCUS AR144763
DEFINITION Sequence 4 fi
ACCESSION AR144763
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US-09-724-797-36 x AR144763
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                                                                        885 CCCCGCGGAGGACCACACCTGGTGCGCGCCCAACGCGGTGGCCCTTCAGGA 934
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167 pValGlyArgThrLeuAspArgGlyAlaSerAlaGluAspMetArgArgG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 lnAspGluProAspHisGlyArgLeuArgGlyValValGlyProAlaPhe 103
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Sequence 4 from patent US 6210935.
AR144763
AR144763.1 GI:15106630
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1620 CCGGAMGCCACGTDCCCC 1637

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sLeu 349 CCTC 1475	3 rgAspProValProSerMetSerPheGlyAlaGlyMetArgTyrCysLeu 	333 1426
31uA 333 ::: CACC 1425	6 aAsnArgAspProArgArgTyrAspArgProAspAspPheAspIleGluA	316 1376
laAl 316 :: CGGC 1375	0 GlyArgArgLeuArgArgAspAspValValValValLeuAlaGlyAlaAl 	300 1326
Arg 299 	3 roSerValGlnSerAsnThrArgGlnLeuAspValAspValGluLeuArg	283 1276
AspP 283 ACC 1275	6 GATGPTOASPLEULEUA1AG1nA1AVA1G1UG1UCYSLEUATGTYTASPP ::: 	266 1226
:gAr 266 	0 AlavalLeuSerLeuLeuAlaHisProAspGlnLeuAspLeuLeuArgAr :::	250 1176
Asn 249 :::: CAGG 1175	3 alThrPheIlePheThrGlyHisGluThrValAlaSerGlnValGlyAsn ::::: :::::::::::::::::::::::::::::	233 1126
7alV 233 GCG 1125	7 aHisAspArgGlyLeuMetSerArgAsnGluIleValSerThrValV :::	217 1076
pA1 217 	1 ArgArgArgArgGluGlyGlyGluAspLeuLeuAlaLeuMetLeuAspAl	201 1026
Ala 200 GAC 1025	4 lyHigAlaAlaIleAlaGluPheAlaAspTyrValGluArgAlaLeuAla ::::: ::: 6 CCGAGGCCGCCTCCCAGGAGTTCACCCGCTACTTCCGGCGAGAGGTGGAC	184 976
111: .casa 975	::::	935

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Sequence Strd Orig ZSCORE ESCORE Len | Documentation | Sequence | Strd Orig ZSCORE | Len | Documentation | Sinsi/gcqdata/geneseq/geneseq-embl/WA1095_DAT: AAQ81792 + 609.00 | 903. | 531851/gcqdata/geneseq/geneseqn-embl/WA2000. DAT: AAAC5535 + 538.50 | 796. | 531851/gcqdata/geneseq/geneseqn-embl/WA2000. DAT: AAC5535 + 538.50 | 796. | 531851/gcqdata/geneseq/geneseqn-embl/WA2000. DAT: AAC55930 + 538.50 | 796. | 531851/gcqdata/geneseq/geneseqn-embl/WA2000. DAT: AAC55930 + 538.50 | 796. | 531851/gcqdata/geneseq/geneseqn-embl/WA2000. DAT: AAC55930 + 508.50 | 746. | 751851/gcqdata/geneseq/geneseqn-embl/WA2000. DAT: AAC55940 + 471.50 | 793. | 751851/gcqdata/geneseq/geneseqn-embl/WA2000. DAT: AAAC55940 + 471.50 | 793. | 751851/gcqdata/geneseq/geneseqn-embl/WA2000. DAT: AAAC55940 + 471.50 | 793. | 751851/gcqdata/geneseq/geneseqn-embl/WA2000. DAT: AAAC55940 + 471.50 | 793. | 751851/gcqdata/geneseq/geneseqn-embl/WA2000. DAT: AAAC95594 + 471.50 | 793. | 751851/gcqdata/geneseq/geneseqn-embl/WA2000. DAT: AAA09569 + 472.50 | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 793. | 
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Database sequences: 1736436
Database length: 858457221
Search time (sec): 210.840000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search information block: Query: US-09-724-797-36 Query length: 402
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-DEV_TIMEOUT=120
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      (HOFF ) HOFFMANN LA ROCHE & CO
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94US-0239430.
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAD14499 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B. subtilis biotin operon and flanking sequences
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alignment_scores:
Quality:
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US-09-724-797-36 x AAQ81792
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ81792 is the B. subtilis biotin operon and flanking sequences, as part of an expression vector it can be used in the recombinant production of biotin (or biotin precursor protein). The biotin can be used as a dietary additive in animal feeds, and as a vitamin supplement for human consumption. Biotin is also useful as a reagent for research, and diagnostic prodcedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biotin genes, and constructs derived from improved production of recombinant biotin use in e.g. dietary supplements
                                                                                                                                                                                                                                                                              104
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                                                                                 154
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                    170
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                  gThrLeuAspArgGlyAlaSerAlaGluAspMetArgArgGlyHisAlaA 187
                                                                              ProAlaAlaAspTrpGlyAlaValGlyArgTrpSerArgAspValGlyAr
                                                                                                                                                                                  TCATTTGCTTGATCAAGTGCAAGGTAAAAAAAAAGATGGAGGTCATTTCGG
                                                                                                                                                                                                               pAspLeuLeuArgProAlaLeuAlaArgGlyAlaMetAspValValAspG
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                                                                                                                   ACTTTGCTTTTCCTTTAGCAAGTTTTGTCATAGCTAACATTATAGGTGTA
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                                                                                                                                                                                                                                                ACGCCGAGAACGACAGAGAGTTATCAGCCGTATATCATTGAAACTGTCCA
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TTGGATTTCGGGCGCTTGAGGAGCTGCCGGTGACTTTT
                                                                         CAGCCTTAATCTT.....GCGGATTTTGAATGGCGGTATCGGCCGCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACGATTGATTTTACCCGCTCAAGAAAGGCATTAACAGAGGGCAATATTA 6033
                                    hrMetPheArgGlyLeuAlaSerLeuProIleAlaPhe
                                                                                                                   oGlyLeuArgLeuGlyCysAlaSerAspAlaLeuAlaTyrGlnProArgT
                                                                                                                                                                   GCACGATTAGAAGCGCAAATTGCGATTAACACTCTTCTGCAGCGAATGCC
                                                                                                                                                                                                     AlaArgThrGlnLeuArgAlaAlaVal...AlaAlaLeuAlaArgLeuPr
                                                                                                                                                                                                                                                 CGCATCTTTCATTCGGGCATGGCCATCATGTTTGCTTAGGGTCCTCGCTG
                                                                                                                                                                                                                                                                                                                                 TAGCATATTCACGAACCCCCGATGTCTTCGATATTACGAGAAGTCCTAATC
                                                                                                                                                                                                                                                                                                                                                       CGTCAAGGAGAACAAGTCTATCTTTTTTTAGGAGCGGCTAATCGAGACCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGACAGCCAGAGTTGCGTCAGAGGATATTGACATCTGCGGGGTGACGATC
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                                                                                                                                                                                                                                                                                      roSerMetSerPheGlyAlaGlyMetArgTyrCysLeuGlySerTyrLeu 353
                                           398
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA75635

seq_documentation_block:
ID AAA75635 standard; DNA;

5970

AAA75635;

22-JAN-2001 (first entry)

Nucleotide sequence of ORF12 which encodes a transcriptional activator.

antibiotic; desosaminyl Narbonolide synthase; polyketide synthase gene; narbonolide polyketide; antibiotic; C12-hydroxyalse; picK; desosamine biosynthesis; picromycin biosynthesis; transferase enzyme; ketolide; beta-glucosidase

Streptomyces

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alignment_block:
US-09-724-797-36 x AAA75635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is used to produce the recombinant DNA compounds CC of the invention. The specification describes a recombinant DNA compound CC expressing recombinant polyketide synthase genes in host cells for the CC production of narbonolide, narbonolide derivatives and polyketides that CC are useful as antibiotics and as intermediates in the synthesis of CC compounds with pharmaceutical value. The DNA compounds may also encode CC a Cl2-hydroxyalse (pick), desosamine biosynthesis and desosaminyl CC transferase enzymes (useful for conversion of ketchides to antibiotics), CC These compounds are also useful for increasing the antibiotic activity CC of a compound relative to the unhydroxylated compound. The recombinant CC host cells are useful as genetic systems that allow rapid engineering CC of the narbonolide polyketide synthase. These would be valuable for CC creating novel ketchide analogs for pharmaceutical applications.
                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAA75635
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                      1472
1607 CGAGGCCGCGCTCAACCACAACATGCTGGAGTCCGACCCGCCGCGGCACA 1656
                                                                           1572 GAC..
                                                                                                                                        1522 TCGGCTACGACCGGGCGCGGCGGTCCTCGCCGATCCCCGGTTCAGCAAG 1571
                                                                                                                                                                                                                                                                                 1422 GATTTCGCGGCCGATCCGTATCCGACGTACGCGAGACTGCGTGCCGAGGG 1471
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20-MAY-1999;
30-APR-1997;
06-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5970 BP; 806 A; 2219 C; 2142 G; 800 T; 3 other;
                               77 aGlu...IleValGlyAspIleIleLeuPheGlnAspGluProAspHisG 93
                                                                                                              61
                                                                                                                                                              44 erArgPheAlaAspValArgAlaValLeuGlyAspGluArgPheAlaArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant pick hydroxylase gene of Streptomyces venezuelae useful for converting ketolides to antibiotics and as antibiotics and intermediates in the synthesis of compounds with pharmaceutical value
                                                                                                                                                                                                                               31 pProValHisArg......GlyAlaHisArgValTrpTyrValS 44
                                                                                                                                                                                                                                                                                                         15 AspValArgArgAspProTyrProSerTyrHisTrpLeuLeuArgHisAs 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Columns 41-44; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashley G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-AUG-1998;
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22-SEP-1998;
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                                                                                              ThrGlyIleArgArgPheTrpThrAspLeuValGlyProGlyLeuLeuAl 77
                                                                                                                                                                                                            TCCGGCCCACCGGGTGCGCACCCCCGAGGGGGACGAGGTGTGGCTGGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-610844/58
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98US-01100880.

99US-011913.

99US-0134990.

97US-0346247.

98US-0073538.

98US-0141908.
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2.216
61.055
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                                                                      TGGCGCAACTCCACGACTCCCCTGACCGAGGC
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387 2535	0 yLeuArgLeuGlyCysAlaSerAspAlaLeuAlaTyrGlnProArgThrM	37 248
370 2485	5 ArgThrGlnLeuArgAlaAlaValAlaAlaLeuAlaArgLeuProGl	35 243
354 2435	8 erMetSerPheGlyAlaGlyMetArgTyrCysLeuGlySerTyrLeuAla :::::: :::::::: ::: ::: 6 ATCTCGCCTTCGGCCACGGCATCCACTTCTGCATCGCGCGCCCCCTTGGCC	238
338 2385	1 gArgTyrAspArgProAspAspPheAspIleGluArgAspProValProS : ::: ::: 6 GCGCTTCCCGGGACCCGCCACCGCTTCGACATCCGCCGGGACACCGCCGGCC	32 233
321 2335	05 ArgAspAspValValValValLeuAlaGlyAlaAlaAsnArgAspProAr	3(228
304 2285	R9 hrargGlnLeuAspValAspValGluLeuArgGlyArgArgLeuArg	21
289 2235	772 aGlnAlaValGluGluCysLeuArgTyrAspProSerValGlnSerAsnT	21
272 2185	6 AlaHisProAspGlnLeuAspLeuLeuArgArgArgProAspLeuLeuAl :::	25 213
255 2135	9 lyHisGluThrValAlaSerGlnValGlyAsnAlaValLeuSerLeuLeu 	23 208
239 2085	22 uMetSerArgAsnGluIleValSerThrValValThrPheIlePheThrG :::::: :::::::::::::::::::::::::::::	20
222 2035	08 GluAspLeuLeuAlaLeuMetLeuAspAlaHisAspArgGlyLe	20 198
207 1985	1 heAlaAspTyrValGluArgAlaLeuAlaArgArgArgArgGluGlyGly::::: ::::	19 193
191 1935	174 gGlyAlaSerAlaGluAspMetArgArgGlyHisAlaAlaIleAlaGluP ::: ::: ::: 886 CTTCGTCCCCGGACGATCCCCGCCCAGGCCCAGACCGCCATGGCCGAGA	17 188
174 1885	158 TrpGlyAlaValGlyArgTrpSerArgAspValGlyArgThrLeuAspAr :::	15 185
157 1856	141 roLeuAlaLeuArgAlaValLeuGlyLeuLeuGlyLeuProAlaAlaAsp 	18
141 1806	126 aLeuAlaArgGlyAlaMetAspValValAspGluLeuAlaTyrp 757 GCTGGCGGCGCCGACCGCGCCGATCTGATGGAGTCCCTGGCCTGGC	1 17
126 1756	110 ArgLeuGluProValIleAlaGlyThrValAspAspLeuLeuArgProAl	1 17
109 1706	93 1yArgLeuArgGlyVa1ValGlyProAlaPheSerProSerAlaLeuArg ::: ::: :::	16

387

etPheArgGlyLeuAlaSerLeuProIleAlaPheThrProGly 401 TGATCCGCGGGCTCAAGGCCCTGCCGATCCGCTGGCGGCGAGGA

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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AA256003
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This is contig 002 from the recombinant cosmid pKOS023-27 DNA sequence (see AA256001) which contains a Streptomyces venezuelae DNA insert. The cosmid contains open reading frames which encode the various modules of the narbonolide polyketide synthase (PKS). The invention relates to recombinant DNA containing a coding sequence for a narbonolide PKS. Polyketides are compounds synthesised from 2-carbon units through a series of condensations and subsequent modifications. Modular PKSs are responsible for the production of many antibiotics including picromycin. The narbonolide PKS consists of a loading module, six extender modules, and two thioester domains. Four proteins make up the narbonolide PKS (PICAI, PICAII, PICAII and PICAIV). PICAI includes the loading module and extender modules 1 and 2, PICAII includes extender modules 3 and 4, PICAIII includes extender modules 3 and 4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Narbonolide polyketide synthase; PKS; cosmid pKOS023–27; contiq
ketolide; amino transferase dehydrase; hydroxylase; picromycin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2000
                                                                                                                                                                                                                                                                                                                    WPI; 2000-072618/06
                                                                                                                                                                                                                                                                                                                                                 Ashley G,
                                                                                                                                                                                                                                                                                                                                                                                                              08-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAY-1999;
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                                                                                                                                                                                                                         Disclosure; Page 35-37; 98pp; English.
                                                                                                                                                                                                                                                                   New recombinant DNA encoding a domain of narbonolide polyketide
                                                                                                                                                                                                                                                                                                                                                                                                                             28-AUG-1998;
22-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from cosmid pKOS023-27 from Streptomyces venezuelae
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                                                                                                                                                                                                                                                                                                                                                                               BIOSCIENCES INC
                                                                                                                                                                                                                                                      production of ketolide antibiotics
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98US-0141908.
98US-0100880.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= PICCIV
/note= "Partial amino transferase-dehydrase"
/transl_except= (Pos:180..182, aa:Xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= transcriptional_activator
/transl_except= (Pos:4818..4820, aa:Xaa)
/note= "Xaa = unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= PicK
/note= "Cytochrome P450 hydroxylase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
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US-09-724-797-36 x AAZ56003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1422 GATTTCGCGGCCGATCCGTATCCGACGTACGCGAGACTGCGTGCCGAGGG
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                                                                                                                                                                                                                                                                                                                                                                                              1757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ThrGlyIleArgArgPheTrpThrAspLeuValGlyProGlyLeuLeuAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 erArgPheAlaAspValArgAlaValLeuGlyAspGluArgPheAlaArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                      aLeuAlaArg.....GlyAlaMetAspValValAspGluLeuAlaTyrP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lyArgLeuArgGlyValValGlyProAlaPheSerProSerAlaLeuArg 109
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TGAGCGGCTATCTCCCCGGCTCATCGACTCCAAGCGCGGGCAGGACGGC
                                                                                                                                                                                                                                                                                                                              roLeuAlaLeuArgAlaValLeuGlyLeuLeuGlyLeuProAlaAlaAsp
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                                           heAlaAspTyrValGluArgAlaLeuAlaArgArgArgArgGluGlyGly
                                                                                              CTTCGTCTTCCCGGACGATCCCGCCCAGGCCCAGACCGCCATGGCCGAGA
                                                                                                                                      \tt gGlyAlaSerAlaGluAspMetArgArgGlyHisAlaAlaIleAlaGluP
                                                                                                                                                                                               CGCGCCGCCTTCCGCGTCTGGACC....
                                                                                                                                                                                                                                       TrpGlyAlaValGlyArgTrpSerArgAspValGlyArgThrLeuAspAr 174
                                                                                                                                                                                                                                                                                                                                                                                              GCTGGCGCCCCGACGCCCCCCCCGATCTGATGGAGTCCCTGGCCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCGGCTGCGCAAGCTGGTGGCCCGTGAGTTCACCATGCGCCGGGTCGAG 1706
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2035

 ${\tt uMetSerArgAsnGluIleValSerThrValValThrPheIlePheThrG}$

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seq_documentation_block:
ID AAZ87301 standard; DN
XX
AC AAZ87301;
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DT 05-JUN-2000 (first e
XX
DE S. venezuelae macroli
XX
DESOsamine biosynthes
KW Desosamine biosynthes
KW biopolymer; antibori
KW chronic obstructive p
KW hypercholesterolaemia
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FT CDS Locat
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                                                                                                                                                                                                                   chronic obstructive pulmonary disease; hypercholesterolaemia; crop protection
                                                                                                                                                                                                                                                                  neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase;
biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ87301 standard; DNA;
                                                                                                                                                                                                                                                                                                                           Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin;

    venezuelae macrolide biosynthetic gene pikC, SEQ ID NO:38.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgThrGlnLeuArgAlaAlaVal...AlaAlaLeuAlaArgLeuProGl 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCTCGCCTTCGGCCACGGCATCCACTTCTGCATCGGCGCCCCCTTGGCC
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                                                                                                                                                                 venezuelae ATCC15439
     /product= "PikC"
/transl_except= (pos:307..309,
                                                            /*tag=
                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                   agent;
                                                                                                                                                                                                                                              respiratory inflammation;
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alignment_block:

US-09-724-797-36 x AAZ87301

Percent Similarity:

Align seg 1/1 to:

AAZ87301

from:

to:

117

TCCGGCCCACCGGGTGCGCACCCCCGAGGGGGACGAGGTGTGGCTGGTCG
erArgPheAlaAspValArgAlaValLeuGlyAspGluArgPheAlaArg

60

31 pProValHisArg.....

67

15 AspValArgArgAspProTyrProSerTyrHisTrpLeuLeuArgHisAs

GATTTCGCGGCCGATCCGTATCCGACGTACGCGAGACTGCGTGCCGAGGG 116

....GlyAlaHisArgValTrpTyrValS 44

alignment_scores:

Quality: Ratio:

531.50 2.196 60.804

Percent Identity:

398 8 34.422

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CC biologically active variant, where the nucleic acid sequence is not considered from the eryC gene cluster of Saccharopolyspora erythraea or CC Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide cC biosynthetic gene cluster encodes proteins which synthesise methymycin, narbomycin or a combination of these cC compounds. Recombinant or augmented cells comprising the desosamine cC proteins are useful for synthesis of methymycin, pikromycin, pikromycin and narbomycin. The alternative termination of polyketide crecombinant host cells are useful as the compounds produced by the cc synthesis may be useful to prepare novel antibiotics and cc recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer pHA monomer synthases or to prepare cC immunosuppressants, agents to treat asthma, chronic obstructive pulmonary chalses as well as other diseases involving respiratory inflammation, cc chieseterol-lowering agents or macrolide-based antibiotics which are castive against a variety of organisms, e.g., bacteria, including cm until-drug resistant pneumococci and other respiratory pathogens, as well cas viral parasitic pathogens or a crop protection agents, as well
                                as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of polyketides in plants. Sequences AAZ87295-Z87302 represent macrolide biosynthetic genes frostreptomyces venezuelae ATCC 15439, which encode proteins AAY77190-Y77197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; Page 428-429; 438pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthesis of methymycin and pikromycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desosamine and macrolide biosynthetic gene clusters, useful for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAY77196
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Sequence 1251 BP;
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                                      erMetSerPheGlyAlaGlyMetArgTyrCysLeuGlySerTyrLeuAla
                                                                                                                                                                                                               ArgAspAspValValValLeuAlaGlyAlaAlaAsnArgAspProAr
                                                                                                                                                                                                                                                                                                    hrargGlnLeuAspValAsp...ValGluLeuArgGlyArgArgLeuArg
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chronic obstructive pulmonary disease; respiratory inflammation;
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Novel nucleic acid molecule comprising mitomycin biosynthetic gene cluster useful for cloning mitomycin biosynthetic genes for elucidating the molecular basis of mitosane ring system biosynthesis

Example 1; Page 255; 399pp; English.

from the mitomycin biosynthetic gene cluster. Mitomycins are a group of natural products that contain a variety of functional groups, including amino benzoquinone and axiridine ring systems. The S. lavendulae mitomycin biosynthetic gene cluster comprises 47 mitomycin genes spanning 55kb of DNA. The invention includes an expression cassette comprising a mitomycin biosynthetic gene operably linked to a promoter, and host cells transformed with the cassette. The nucleotide, and protein sequences and the transformed host cells of the invention result in antiasthmatic, antiinflammatory, cytostatic, immunomodulatory, and antibiotic activities. The nucleotide sequences are used to elucidate the molecular basis for the biosynthesis of the mitosane ring system, as well as to engineer the biosynthesis of novel natural products, e.g. immune-enhancers, immunosuppressants, agents to treat asthma, obstructive pulmonary disease as well as other disease involvinespiratory inflammation, or cholesterol-lowering agents or as antibiotics, anti-inflammatory agents, anti-cancer agents invention relates to isolated and purified nucleic acid molecules

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                                                                                                                                                                                                                                         Staurosporin; gene cluster; indole-carbazole alkaloid; ICA; antibiotic; antiproliferative; platelet aggregation; fungus; yeast; Ca2+/phospholipid-dependent serine/threonine protein kinase; ds.
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                                                                                                                                                                                                    longisporoflavus (strain R19)
                                                                                                                                                                                                                                                                                                                                                                          (first
  /*tag= a /label= Gene_1 /note= "Encodes a protein containing 1747...2553
                                                                                                                                     378..165
                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                          entry)
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                                                                     425 amino acids"
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alignment_scores:
Quality:
                                                                                                                              alignment_block:
US-09-724-797-36 x AAT70153
                                                                                                                                                                                                                                                                                                 The present sequence represents the 6.5kb PvuII fragment of Streptomyces CC longisporoflavus R19 which is involved in the biosynthesis of CC indole-carbazole alkalolis (ICA). The sequence contains five functional CC fragments as indicated in the features table. The DNA or a hybrid CC vector containing it can be used to prepare an ICA or derivatives and CC precursors, either by allowing production in previously incapable CC organisms or by improving yields. In particular, the antibiotic CC staurosporin can be produced. Staurosporin is known to have inhibitory CC activity against fungl, yeasts, and Cc2+/phospholipid-dependent CC setine/threonine protein kinases (PKCs). Staurosporin also has CC antiproliferative activity and can inhibit platelet aggregation. CC The present sequence can also inactivate ICA biosynthesis genes and CC can be used in PCR amplification. An advantage of this is that CC productivity of staurosporin-synthesising Streptomyces is improved CC over natural strains yielding only low concentrations.
                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                              Align seg 1/1 to: AAT70153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bietenhader J, Engel N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 37-41; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CIBA ) CIBA GEIGY AG
                                 441 CCCTACCCGGTCTACCGGGCGCTACCGGGAGGCCGCCCCGGTCCATCGCAC 490
                                                                                                                                                                                                                                                                      Sequence 6085 BP; 882 A; 2374 C; 1992 G; 833 T; 4 other;
                                                         20 ProTyrProSerTyrHisTrpLeuLeuArgHisAspProValHisArg..
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95EP-0810534.
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/label= Gene_5_(part)
/label= Gene_5_(part)
/note= "Partial sequence for gene 5; full length
/note= "protein contains 366 amino acids and is
significantly similar to amino transferase
enzymes, such as the Dnr J protein"
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/note= "Encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Gene_3
/note= "Encodes a
                                                                                                                                                                             508.50
2.101
59.459
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                                                                                                 from: 1
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                                                                                                                                                               Length: 407
Gaps: 11
Percent Identity: 36.364
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                                                                                                 to: 6085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schupp T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   containing 328 amino acids"
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316	300 1326	283 1276	266 1226	250 1176	233 1126	217 1076	201 1026	184 976	167 935	154 885	137 835	120 785	104 735	87 685	75 635	65 585	48 541	491
6 aAsnArgAspProArgArgTyrAspArgProAspAspPheAspIleGluA 3	O GlyArgArgLeuArgArgAspAspValValValValLeuAlaGlyAlaAl 3 ::: :::	roSerValGlnSerAsnThrArgGlnLe	5 gArgProAspLeuLeuAlaGlnAlaValGluGluCysLeuArgTyrAspP 2) AlaValLeuSerLeuLeuAlaHisProAspGlnLeuAspLeuLeuArgAr 2 :::	alThrPheIlePheThrGlyHisGluThrValAlaSerGlnValGlyAsn 2	aHisAspArgGlyLeuMetSerArgAsnGluIleValSerThrValV 2	ArgArgArgGluGlyGlyGluAspLeuLeuAlaLeuMetLeuAspAl 2	. lyHisAlaAlaIleAlaGluPheAlaAspTyrValGluArgAlaLeuAla 20 ::::: CCGAGGCGGCGTCCCAGGAGTTCACCCGCTACTTCCGGCGAGAGGTGGAC 10	PValGlyArgThrLeuAspArgGlyAlaSerAlaGluAspMetArgArgG 1 ::::	.ProAlaAlaAspTrpGlyAlaValGlyArgTrpSerArgAs 16	luLeuAlaTyrProLeuAlaLeuArgAlaValLeuGlyLeuLeuGlyLeu 1 ;;;;;;;;;; ;;; gTTCGCGGCGCCCCCCCGGATCCTCGTCATCTCCGCACTGCTGGGCATC	paspLeuLeuargProAlaLeualaargGlyAlaMetAspValValAspG 137 :::: cGAACTCCTGGACCGGCTCCGAGCACCACCGCCCGGCCCG	SerProSerAlaLeuArgArgLeuGluProValIleAlaGlyThrValAs 12	GlyProAlaPhe 1 ACCGGCGAGTTC 7	LeuLeuAlaGluIleValGlyAspIleIleLeuPheG 87	ArgPheTrpThrAspLeuValGlyProGly	spValArgAlaValLeuGlyAspGluArgPheAlaArgThrGlyIleArg 64 :::::: :::::: ACGTGGTCCGCGTCCTGTCCAACCGGCGGTTCGGCCGCAACGCC 58	GCGGCGGGCCCGGAAAGCCTGACCTACTACGTGTTCACCTACGACG 54
ω ω		99 325	83 275	66 225	175	33 125	17 075	00	84	67	153 884	34	84	03 34	4	4	4	0

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seq_documentation_block:
ID AAC55840 standard; DN
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AC AAC55840;
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Mitomycin; blosynthes
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                            This invention relates to isolated and purified nucleic acid molecules from the mitomycin biosynthetic gene cluster. Mitomycins are a group of natural products that contain a variety of functional groups, including amino benzoquinone and axiridine ring systems. The S. lavendulae mitomycin biosynthetic gene cluster comprises 47 mitomycin genes spanning 55kb of DNA. The invention includes an expression cassette comprising a mitomycin biosynthetic gene operably linked to a promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitomycin; biosynthesis; mitosane ring system; antibiotic; anti-cancer; anti-inflammatory; immune-enhancer; immunosuppressant; asthma; chronic obstructive pulmonary disease; respiratory inflammation;
                                                                                                                                                                                                                                                                                                                     Novel nucleic acid molecule comprising mitomycin biosynthetic gene cluster useful for cloning mitomycin biosynthetic genes for elucidathe molecular basis of mitosane ring system biosynthesis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces lavendulae
                                                                                                                                                                                                                                                                      Claim 26; Figure 22;
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      host cells transformed with the
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      and protein
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibiotics, anti-inflammatory agents, anti-cancer agents, immune-enhancers, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other disease involving respiratory inflammation, or cholesterol-lowering agents or as crop protection agents (e.g. fungicides or insecticides) as well as protection agents (e.g. fungicides or insecticides) as well as bipolymers, e.g., in packaging or biomedical applications, or to engineer PHA monomer synthases. Sequences AAC55782-C55881, AAC55815-C55849 and AAB32485-B32542 represent mitomycin biosynthetic gene cluster DNA sequences and encoded proteins. Sequences AAC55812-C55814, AAC55850-C55855 and AAC55862-C55869 represent PCR primers used in the cloning of the mitomycin biosynthetic genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequences and the transformed host cells of the invention result in antiasthmatic, antinflammatory, cytostatic, immunomodulatory, and antibiotic activities. The nucleotide sequences are used to elucidate the molecular basis for the biosynthesis of the mitosane ring system, as well as to engineer the biosynthesis of novel natural products, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12249
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seq_documentation_block:
ID AAC55857 standard; DNA; 18
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AC AAC55857;
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DT 19-JAN-2001 (first entry:
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Complete nucleotide sequent
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Mitomycin; biosynthesis; n
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KW anti-inflammatory; immune
KW chronic obstructive pulmon
KW chronic obstructive pulmon
KW fungicide; pesticide; ds.
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                                          Mitomycin; biosynthesis; mitosane ring system; antibiotic; anti-cancer; anti-inflammatory; immune-enhancer; immunosuppressant; asthma; chronic obstructive pulmonary disease; respiratory inflammation;
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alignment_block: US-09-724-797-36 x AAC55857

Percent Similarity:

Percent

Identity:

Gaps:

8 33.085

Align seg 1/1 to: AAC55857

from: 1

to: 18331

8638

27

GCGCCGCGAGCGGCCGCTGCAACGCGTCACGCTGCCGTACGGCGGCGAGG uLeuArgHisAspProValHisArg......GlyAlaHisArgV CCCTTCCACGCCCCGACCGGCTGGAGCCCGACCCGTACTGGGAGCCGCT ProThrAspAlaAspValArgArgAspProTyrProSerTyrHisTrpLe

8737 40 8687 27

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alignment_scores:
                                                                                                                                                      CC from the mitomycin biosynthetic gene cluster. Mitomycing are a group of contral products that contain a variety of functional groups, including amino benzoquinone and axiridine ring systems. The S. lavendule comprising a mitomycin biosynthetic gene cluster comprises 47 mitomycin genes comprising a mitomycin biosynthetic gene cluster comprises 47 mitomycin genes comprising a mitomycin biosynthetic gene operably linked to a promoter, can host cells transformed with the cassette. The nucleotide, and protein cantibiotic activities. The nucleotide sequences are used to elucidate the cantibiotics, anti-inflammatory, cytostatic, immunomodulatory, and cantibiotics, anti-inflammatory agents of the mitosane ring system, as well as to engineer the biosynthesis of novel natural products, e.g. cantibiotics, anti-inflammatory agents, anti-cancer agents, chronic constructive pulmonary disease as well as other disease involving crespiratory inflammation, or cholesterol-lowering agents or as crop protection agents (e.g. fungicides or insecticides) as well as comparation as well as other disease involving crespiratory inflammation, or cholesterol-lowering agents or to engineer bipolymers, e.g., in packaging or biomedical applications, or to engineer comparatory and encoded proteins. Sequences AAC55812-C55849 and CC AAB32485-B3342 represent mitomycin biosynthetic gene cluster DNA calculation of the mitomycin biosynthetic genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acid molecule comprising mitomycin biosynthetic gene cluster useful for cloning mitomycin biosynthetic genes for elucidating the molecular basis of mitosane ring system biosynthesis \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SHER/)
(MAOY/)
(VARO/)
                                                                                                             Sequence 18331 BP; 2523 A;
                                                                                                                                              cloning of the mitomycin biosynthetic genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-601980/57.
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                                                           CCATCGGCACCGTGGACGGCTTTCCCCCGTACGGCCACCGAGGACGTCGAG
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                                                                                                          CTCGGGGGAGTCCTGGTCAGGGCCGGGGAGACGGTCGTGCCGTCGATGGG
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                                    CGCCGCCAACCGCGACCCCGAGCTGTTCACGGACCCCGACGAGCTGGACC 9598
                                                                                                                                             LeuArgGlyArgArgLeuArgArgAspAspValValValLeuAlaGl 314
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                     Bacteria signal to one another to coordinate expression of specific genes in a cell density dependent fashion. This "bacterial signalling" is called "quorum sensing and response". Quorum sensing allows a bacterial species to sense its own number and regulate gene expression according to population density. The present sequence is an open reading frame (ORF) of a Pseudomonas aeruginosa quorum sensing controlled gene. Inhibitors of quorum sensing signalling renders a bacterial population more susceptible to treatment. The present invention relates to a method for identifying modulators of quorum sensing signalling in Pseudomonas aeruginosa bacteria. Modulators of quorum signalling in Pseudomonas aeruginosa bacteria infections. P. aeruginosa is an opportunistic pathogen of immunocompromised individuals (burn patients, cystic fibrosis patients, patients undergoing immunosuppressive therapy and patients with AIDS).
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                                                                                                                                                                                                                                                                                       Claim 46; Page 101-102; 115pp; English
                                                                                                                                                                                                                                                                                                                                             Identifying modulators of quorum sensing signaling in Pseudomonas aeruginosa bacteria, useful for treating infections in
                                                                                                                                                                                                                                                                                                                                                                                                                                         Whiteley M, Lee KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-SEP-1999;
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA09469
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ID AAA09469 standard;
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/*tag= c
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5772..18224
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29787..40346
                                                       /product= 8,8a-deoxyoleandolide_synthase_3
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18267..29717
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This is part of the Streptococcus antibioticus oleandomycin gene cluster. C The oleandolide polyketide synthase (PKS), also known as C (ORF), designated oleal, olealI and olealII. The PKS is a type I C "modular" enzyme, where each ORF encodes 2 extender modules and the first ORF also encodes the loading module. Each module is composed of at least a ketosynthase (KS), acyl-transferase (AT) and an acyl carrier protein (ACP) domain. The oleandolide PKS loading module contains an inactivated KS, called KS-0, where 0 is the abbreviation for a cyl carrier protein (ACP) domain. The oleandolide PKS loading module contains an inactivated KS, called KS-0, where 0 is the abbreviation for glutamine, present instead of the active site cysteine required for composed decarboxylative condensations between acylthicesters followed by cycles of polyketide macrolactones through multistep pathways involving composed decarboxylation concerns an isolated recombinant DNA compound, comprising a glycosylation to yield oleandomycin, an antibacterial polyketide. The modules 1-4 or 1-6, including an oleandolide PKS operably linked to a promoter. Also discussed are recombinant DNA compound, comprising a promoter. Also discussed are recombinant oleandolide PKS in which the particular, the inactivation is mediated by a change in the KS domain of that renders it incapable of binding substrate (the KS1-0 mutation), crendered by mutation in the codon for the active site cysteine. The cleandolide PKS is asserbly ensemble of conditions and motilides. Heterologous expression of oleandolide PKS in which have useful for synthesizing polyketides, which are useful cas antibiotics and motilides. Heterologous expression of oleandolide PKS corresponding derivatives of erythromycins A-D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant DNA compound encoding oleandolide polyketide synthase for synthesizing polyketides comprising a coding sequence for a domain of a loading module or any one of extender modules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 14-26; 86pp; English.
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P-PSDB; AAY92707, AAY92708, AAY92709.
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16-FEB-1999;
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                                           47173 ACCTGACCAAGGGCGAGATCGTCAACATGGGGGTGAGCCTGCTCATCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46621 GCCTGCCCTACGGCGAGGGCACGGCCTGGCTGGTCACCCGCATGTCCGAC
                                                                                                                                                                                                                                                           190 GluPheAlaAspTyrValGluArgAlaLeuAlaArgArgArgArgGluGl
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                                                                                                                                                                                                                                                                                                                                             174 ..ArgGlyAlaSerAlaGluAspMetArgArgGlyHisAlaAlaIleAla 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147
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GlyHisGluThrValAlaSerGlnValGlyAsnAlaValLeuSerLeuLe
                                                                          euMetSerArgAsnGluIleValSerThrValValThrPheIlePheThr 238
                                                                                                                              CACCGAGGACCTGCTCGCCCTCGCCACCGACCACCGACGACC
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                                                                                                                                                                       yGlyGluAspLeuLeu...AlaLeuMetLeuAspAlaHisAspArgGlyL 222
                                                                                                                                                                                                                                                                                                                                                                                                                 ValLeuGlyLeuGlyLeuProAlaAlaAspTrpGlyAlaValGlyAr 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CACCCGCCGACCTGGTCGAGTTCCTCGCCGTTCCCCTTCCCCGTCGCGGTC
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seq_documentation_block:
ID AAQ73674 standard; DNA; 2168 BP
XX AAQ73674;
XX 21-JUN-1995 (first entry)
XX
DT 21-JUN-1995 (first entry)
XX
Mycinamicin; hydroxylase; macro
XX
Mycinamicin; hydroxylase; macro
XX
Micromonospora griseorubida; ds
XX
OS Micromonospora griseorubida AT1
XX
CDS Location/Qualif
FH Key 152..1442
FT CDS 252..1442
FT CDS /*tag= a
FT XX
PD J906253853-A.
XX
D9-MAR-1993; 93JP-0047638.
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PF 09-MAR-1993; 93JP-0047638.
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PR (ASAH) ASAHI KASEI KGGYO KK.
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                                                                                                                                                                                                                                                                                                                                                                                  Mycinamicin; hydroxylase; macrolide; antibiotic; Micromonospora;
                                                                                                                                                                                                                                                                                                                                                                                                                         Mycinamicin IV hydroxylating protein gene sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGCGGCGGTGGAGAGATGCTGCGGTACACACCGCTGGTGTCCGCCGGC 47372
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alignment_block:
US-09-724-797-36 x AAQ73674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The DNA sequence of a gene encoding a protein having mycinamicin IV hydroxylase (MH) activity. The gene encodes a protein of 396 a.a. The DNA was obtained from the macrolide antibiotic-producing bacterium Micromonospora griseorubida AAA11725CN3/pTYS507. The gene was isolated from the plasmid pTYS507. The protein encoded by this plasmid can be used to produce mycinamicin IV in pTYS507-deficient Micromonospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2168 BP; 331 A;
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P-PSDB; AAR60777.
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                                                                                             ProLeuAlaLeuArgAlaValLeuGlyLeuLeuGlyLeuProAlaAlaAs
                                                                                                                                                                roAlaLeuAlaArgGly...AlaMetAspValValAspGluLeuAlaTyr 140
                                                                                                                                                                                                                                                                                        CACAGCCGATTGCGCCGACTCGTCGTCAAGGCGTTCACCGCCCGTCGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                 pTrpGlyAlaValGlyArgTrpSerArgAspValGlyArgThrLeuAspA 174
                                                                                                                                                                                                                 GGAGTCGCTGCGCGCGTGCCCGCGAGATCGCGCACGAGCTGGTCGATC
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CCACGACCGCTTCACCCGGTGGTCCGGGGCCTTCCTCCTCCACCGCCGAG.

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FH XXX DE XXX DE XXX DE XXX
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AAI71296 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....ArgGlnLeuAspValAspValGluLeuArgGlyArgArgLeuAr 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGACCGGAGCTGCGTCGACAGCTACTCGATCGGCCGGAGCTGATTCCGT 1053
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                                                                                                                                                                  (first entry)
                                                                                                                    griseus RppA protein encoding DNA
                                         griseus.
                                                                               griseus;
Location/Qualifiers
                                                                          RppA; pyran-2-one; drug; agricultural;
                                                                                                                                                                                                                                                                                                                                                      1439
                                                                                                                      SEQ ID NO:1.
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alignment_block:
US-09-724-797-36 x AAI71296
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                               574 C.....CCCCGGATGACCCCGGAGCCGATCGTGCAGG
                                                                                                                                                                                                           524
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                                                                                                                                                                                                                                                                                                                                                   424
                                                                                                                                                                                                                                                                                                                                                                                                                    374 GTCCGGAACTGTCCTTTCGACTACGCGCACGAGCTGGAGTTCGACCCCCA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes the preparation of pyran-2-one derivatives. The preparation method comprises contacting carbonyl compounds with microbes containing a polyketide synthase gene. Pyran-2-one derivatives can be used as synthetic intermediates for drugs and agricultural chemicals. They can also be used as additives for thermosensible transfer paper. The present sequence encodes the specifically claimed Streptomyces griseus RppA protein, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preparation of pyran-2-one derivative, used as intermediate and as additive for thermosensible transfer paper, comprises contacting carbonyl compound with microbe containing polyketide synthase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2795 BP; 435 A; 1051 C; 908 G; 401 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 7-8; llpp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAG68148
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                                                                                                                                                                                                                                                                                                                                                                    16 ValArgArgAspProTyr......proSe
                                                                                                                                                                                                                           ValLeuGlyAspGluArgPheAlaArgThrGlyIle.....ArgArgPh
CTGGTGGCCAAGAGCTTCACCCCG
                         ValValGlyProAlaPheSerProSerAlaLeuArgArgLeuGluProVa 114
                                                                                              lyAspIleIleLeuPheGlnAspGluProAspHisGlyArgLeuArgGly 97
                                                                                                                                                                  eTrpThrAspLeuValGlyProGlyLeuLeuAlaGlu.....IleValG
                                                                                                                                                                                                                                                                           ACGGAGAGGCCAGGCCTGGCTGGTCACCCGCTACGAGGACGTCCGGACG
                                                                                                                                                                                                                                                                                                         ...GlyAlaHisArgValTrpTyrValSerArgPheAlaAspValArgAla
                                                                                                                                                                                                                                                                                                                                              GCTCAGGCAATTGCTCACCGAGGAGCCGGTGTCCCGCATCCGTATGGCGT
                                                                                                                                                                                                     GTCACCACCGACCGGCGGTTCAGCCGCAGCGCCGTCCTCGGCCGGGACTT
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/product= "RppA protein"
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_documentation_block: AAF81954 standard;

DNA;

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18-JUN-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 lIleAlaGlyThr......ValAspAspLeuLeuArgProAlaLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lyAlaSerAlaGluAspMetArgArgGlyHisAlaAlaIleAlaGluPhe 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGAGGGCTCACCGGGCGACTTCGTCGCCCGGGTCTCCGCGCGCCGCTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gArgAspAspValValValLeuAlaGlyAlaAlaAsnArgAspProA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACACCACGACCTACCAGCTCGGCAACATCGCCTACACCCTGCTCACCCG 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluThrValAlaSerGlnValGlyAsnAlaValLeuSerLeuLeuAlaHi 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGACGACGACGCCGTCATGGCGATGGTCCTGCTCATCACCGGCCAG 1075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uAspLeuLeuAlaLeuMetLeuAspAlaHisAspArgGly...LeuMetS
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                                                                                         CCCTGCGTCTGGACGTGCCGCCCGAGGACGTCTCGTGGAACACGACGTCC
                                                                                                                                                                                  CACCATGGAGCTGGAAGTGGCCTTCTCCACGCTGCTGACCCGCTTCCCGG
                                                                                                                                                                                                                            aArgThrGlnLeuArgAlaAlaValAlaAla...LeuAlaArgLeuProG 370
                                                                                                                                                                                                                                                                                  CACATGACGTTCGGCTGGGCGCCCCACCACTGCCTGGGCGCGCCGCTGGC
                                                                                                                                                                                                                                                                                                                            SerMetSerPheGlyAlaGlyMetArgTyrCysLeuGlySerTyrLeuAl 354
                                                                                                                                                                                                                                                                                                                                                                            CCAAGTTCGACCGTCCCGACGACGTGGACCCGACCGGCCGACCATCCCC
                                                                                                                                                                                                                                                                                                                                                                                                       rgArgTyrAspArgProAspAspPheAspIleGluArgAspProValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCCGGCGACGTGCCACGTGTCCTACCTGACGGCCAACCGGGACTCCG 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCCGTATCGCCCTGGAG...GACGTGGAGCTCTCCGGCGTCCTCATCAA
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ATCTGGCGTTACCCGCCTCGCCCTGCCCGTCACATGG
                                          MetPheArgGlyLeuAlaSerLeuProIleAlaPhe
                                                                                                                                     lyLeuArgLeuGlyCysAlaSerAspAlaLeuAlaTyrGlnProArgThr
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:AAF81954
                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-724-797-36 x AAF81954
                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                        Align seg 1/1 to: AAF81954
                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a method for preparing 1,3,6,8-tetrahydroxynaphthalene comprising using a microbe cell containing an rppA gene encoding actinomycetes polyketide synthase, to convert malonyl CoA as the substrate or a substance which can produce malonyl CoA in the microbe cell to 1,3,6,8-tetrahydroxynaphthalene and recovering it. 1,3,6,8-tetrahydroxynaphthalene is used as a synthetic material for melanine and as an intermediate for drugs and agricultural chemicals. The present sequence encodes the actinomycetes polyketide synthase protein isolated from Streptomyces griseus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preparation of 1,3,6,8-tetrahydroxynaphthalene for use as a synthetic material for melanine and as an intermediate for drugs and agricultural chemicals, comprises using a microbe and an enzyme \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        malonyl CoA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces griseus actinomycetes polyketide synthase encoding DNA
                                                 424
                                                                                                             374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 6-7; 10pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces griseus; actinomycete; 1,3,6,8-tetrahydroxynaphthalene; meJ
                                                                                                                                                                                                                                                                                                                                          Sequence 2795 BP; 435 A;
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                                                                                                                                        ..GlyAlaHisArgValTrpTyrValSerArgPheAlaAspValArgAla
                                                  GCTCAGGCAATTGCTCACCGAGGAGCCGGTGTCCCGCATCCGTATGGCGT
                                                                    GTCCGGAACTGTCCTTTCGACTACGCGCACGAGCTGGAGTTCGACCCCCA 423
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                                                                                                                                                                                                                                                                                                                                          1051 C;
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                                                                                                                                                                                                                                                   Percent
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melanine; agricultural chemical;
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CCAAGTTCGACCGTCCCGACGAGCTGGACCCGACCGGCCGACCATCCCC
                           rgArgTyrAspArgProAspAspPheAspIleGluArgAspProValPro 337
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                                                                                                                                                                        CCCCGTATCGCCCTGGAG....GACGTGGAGCTCTCCGGCGTCCTCATCAA
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:AAQ14548
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                                                                                           The eryF gene encodes the 6-hydroxylase component of the cytochrome P450 monooxygenase system responsible for the hydroxylation of 6-de-oxyerythronolide B to erythronolide B. Interruption of this step results in the formation of deoxyerythromycin A and new derivatives useful as antibiotic which have better stability against acids that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354
                        the corresponding erythromycins. Interruption of the reaction can be effected by an insertion into the eryF gene of a plasmid, gene replacement or chemical or light-induced mutagenesis. The gene is positioned between the eryH and eryG genes. See also AAQ14549.
                                                                                                                                                                                                         New 6-deoxy:erythromycin acid stability, produced
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saccharopolyspora;
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Sequence 1400 BP;
                                                                                                                                                                                 Disclosure; Fig 3; 56pp; English.
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alignment_scores

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246 nValGlyAsnAlaValLeuSerLeuLeuAlaHisProAspGlnLeuAspL 263
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                                                                                                                                TCAGGGTCCAGGACGACGATGACGGTCGGCTCAGCGCCGACGAGCTGTCC
                                                                                                                                                                   euAspAlaHis.....AspArgGlyLeuMetSerArgAsnGluIleVal 229
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                                                                                     SerThrValValThrPheIlePheThrGlyHisGluThrValAlaSerGl 246
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                                             TCCATCGCGCTGCTGCTGCTGGCCGGTTTCGAGGCGTCGGTGAGCCT 903
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seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA95667
                                                                                                                                                                                                                                  1354 GGTGCGGCTCGACGGATGAGCACCTGGC 1381
                                                                                                                                          1304 GACGTGGTGTGGCGGCGTTCGGTGCTGCTGCGGGGCATCGACCTACC
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                                                                                                                                                                                      AlaLeuAlaTyrGlnProArgThrMetPheArgGlyLeuAlaSerLeuPr 395
                                                                                                                                                                                                                                                                                                                              CTTCTGCATGGGCCGGCCGCTGGCCAAGCTGGAGGGCGAGGTGGCGCTGC
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Bacillus subtilis hydroxylating enzyme gene

Hydroxylated bicyclic compound; lactone; HMG-CoA; inhibitor; ds; hydroxymethylglutaryl co-enzyme A reductase; hypocholesterolaemia

Mizoguchi H, Hashimoto Ś Ozaki

seq_documentation_block:
ID AAA95667;
XX AAA95667;
XX AAA95667;
XX 14-FEB-2001 (first entry)
XX Bacillus subtilis hydroxylating
XX hydroxylated bicyclic compound;
XX Hydroxylated bicyclic compound;
XX Hydroxymethylglutaryl co-enzyme
XX AAA95667;
XX Bacillus subtilis.
XX Bacillus subtilis hydroxylated bicycl
AAA95667;
ABAA95667;
ABAA9667;
ABAA9 New protein derived from Bacillus genus microorganism useful for producing a hydroxylated bicyclic compound e.g. ${\tt HMG\textsc{-}COA}$ reductase inhibitors

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alignment_scores:
Quality:
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US-09-724-797-36 x AAA95667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAA95667 from: 1 to: 1204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the coding region for a novel Bacillus derived protein having the activity of producing a hydroxylated bicyclic compound or the corresponding lactone from a bicyclic compound or the corresponding lactone. The protein is used for preparing hydroxylated compounds useful as hydroxymethylglutaryl co-enzyme A (HMG-COA) reductase inhibitors and hypocholesterolaemic agents.
                                                                                                                                                                                                                                                                                                                                453
                                                                                                                                                                                                                                                                                                                                                                                                                   403 TCACGATTTTCATACCCGCTTCCGGTTATTGTGATATCTGAGCTGCTGG
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                                                                                                                                                                                                                            500 CTGGTCAGTACACCGAAGGATAAAAGTGAAGAAGCTGAA.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Page 90-94; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 TAACATGGACCCGCCGAAGCATACAAAAATCCGTTCAGTCGTGAACAAAG 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 TGAAGAAAACCAAGTGTGGAGCGTTTTTCTTTATGATGATGTCAAAAAAG 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35 gGlyAlaHisArgValTrpTyrValSerArgPheAlaAspValArgAlaV 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 CCGTTTCCATGGTATGAATCGATGAGAAAGGATGCGCCTGTTTCCTTTGA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 ProTyrProSerTyrHisTrpLeuLeuArgHisAspProVal...HisAr
AspLeuLeuAlaLeuMetLeuAspAlaHisAspArgGly...LeuMetSe 224
                                             gGlyHisAlaAlaIleAlaGluPheAlaAspTyrValGluArgAlaLeuA 200
                                                                                                                                                                                                                                                          ...ValGlyArgThrLeuAspArgGlyAlaSerAlaGluAspMetArgAr 183
                                                                                                                                                                                                                                                                                                                           GAGTGCCTTCAGCGCATATGGAACAGTTTAAAGCATGGTCT...GATCTT 499
                                                                                                                                                                                                                                                                                                                                                                   lyLeuProAlaAlaAspTrpGlyAlaValGlyArgTrpSerArgAsp...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspLeuValGlyProGlyLeuLeuAlaGluIleValGlyAspIleIleLe 85
                                                                                                                                         .....AAAGCCTTTTTGGAAGAACGAGATAAGTGTGAGGAAGAACTGG
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Percent Identity: 30.447
                                                                                          ....ArgArgArgArgGluGlyGlyGlu 208
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Sequence Strd Orig ZSCORE LEN | Documentation | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 | 1,000 
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Database sequences: 383533
Database length: 122816752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM of: US-09-724-797-36 to: Issued_Patents_NA:*
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-DB=Issued_Patents_Na -QFWF=fastap -SUFFIX=rni -GAPOP=12.000
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-FGAPOP=6.000 -FGAPEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -EDELEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -XGAPOP=10.000 -YGAPEXT=0.500
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-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09724797_@CGN1_1116 -NCPU=6 -ICPU=3 -LONGLOG
-NORM=ext -ANDE -LONGLOG
-NORM=ext -ANDE -LONGLOG
-NORM=-XINDER -XINDER -X
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alignment_block: US-09-724-797-36 x
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                                                                                                                                                                                           Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08676818 Patent No. 6057136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/239
FILING DATE: May 6, 1994
APPLICATION NUMBER: 08/084
FILING DATE: June 25, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                               5493 GCATCGTCAACTGCATCTTCTGAGTTTTTGAAAAACCCATATTCTTTTTA 5542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PS/2 Model 50z or 55s:
OPERATING SYSTEM: MS-DOS (Version 5
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: BIOTIN BIOSYNTHESIS IN BACILLUS TITLE OF INVENTION: SUBTILIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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24 rHisTrpLeuLeuArgHisAspProValHisArgGlyAla......
                                                                                                                        8 AlaPheAspProThrAspAlaAspValArgArgAspProTyrProSerTy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 08-JUJ CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
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Pero, Janice G.
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6434 TAGCATATTCACGAACCCCGATGTCTTCGATATTACGAGAAGTCCTAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6034 TGGCTGTGCAGGCTATGGCATATTTCAAAGAGCTGATTCAAAAGAGAAAA 6083
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                                                  oArgArgTyrAspArgProAspAspPheAspIleGluArgAspProValP 337
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                                                                                                                                                                     ArgArgAspAspValValValValLeuAlaGlyAlaAlaAsnArgAspPr 320
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GENERAL INFORMATION:
APPLICANT: Bower, Stanley Grant
APPLICANT: Perkins, John B.
APPLICANT: Yocum, R. Rogers
APPLICANT: Yocum, S. Rogers
INVENTION: BIOTIN BIOSYNTHESIS IN
TITLE OF INVENTION: SUBTILIS
TITLE OF INVENTION: SUBTILIS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                        US-09-407-549-1
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                                                            alignment_scores:
    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6303377
                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                      NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 0459
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6534 GCACGATTAGAAGCGCAAATTGCGATTAACACTCTTCTGCAGCGAATGCC
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS- Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: June 25, 19 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                     TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/239
FILING DATE: May 6, 1994
APPLICATION NUMBER: 08/084
FILING DATE: June 22/193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/407,549 FILING DATE:
                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                      TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                      Quality:
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                                                                                                                                                                nucleic acid
EDNESS: double
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Percent Identity: 33.586
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alignment_block:
US-09-724-797-36 x US-09-407-549-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55
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heThrGlyHisGluThrValAlaSerGlnValGlyAsnAlaValLeuSer
                                                                                                                                                                                                                                                                GGATAAGCTGACGGAAGGAGGCGGCATCTACGTGCATATTGCTGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGCTGTGCAGGCTATGGCATATTTCAAAGAGCTGATTCAAAAGAGAAAA
                                                                                                                   LeuLeuAlaHisProAspGlnLeuAspLeuLeuArgArgArgProAspLe 270
                                                                                                                                                                           TCGCCGGACATGAGACAACGGTCAATCTCATCAGCAATTCAGTCCTTTGT 6233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACGATTGATTTTACCCGCTCAAGAAAGGCATTAACAGAGGGCAATATTA 6033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pAspLeuLeuArgProAlaLeuAlaArgGlyAlaMetAspValValAspG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SerProSerAlaLeuArgArgLeuGluProValIleAlaGlyThrValAs 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGCGAGATTCAAAGTCCGCACCCCGCTGCCTGAGAGCTCAACCAAATA 5692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCATCGTCAACTGCATCTTCTGAGTTTTTGAAAAACCCCATATTCTTTTTA 5542
                                                                                       CTGCTGCAGCATCCAGAACAGCTTTTGAAACTGAGAAAATCCAGATCT
                                                                                                                                                                                                                                                                                                            gGlyLeuMetSerArgAsnGluIleValSerThrValValThrPheIleP 237
                                                                                                                                                                                                                                                                                                                                                      CGCCACCCTCAACAGGATATGATCAGCATGCTCTTGAAGGGGAGAGAAAA 6133
                                                                                                                                                                                                                                                                                                                                                                                               ArgGluGlyGlyGluAspLeuLeuAlaLeuMetLeuAspAlaHisAspAr 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProAlaAlaAspTrpGlyAlaValGlyArgTrpSerArgAspValGlyAr 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAACCAGCCTGATCATAGACGATTGCGGACGCTTGCCAGCGGAGCGTTT 5783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAGGAC.....CTTTCACATGTGCAAAATCAAATGATGCTGTTTC 5733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCCGGGCTGGTATGTCACAGGATATGAAGAAACGGCTGCTATTTTGAAA 5642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isArgValTrpTyrValSerArgPheAlaAspValArgAlaValLeuGly 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGACACATTGCGAGCTGTTCATCCTATCTATAAAGGGAGTTTCTTAAAAT 5592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  laIleAlaGluPheAlaAspTyrValGluArgAlaLeuAlaArgArgArg 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gThrLeuAspArgGlyAlaSerAlaGluAspMetArgArgGlyHisAlaA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTITICCTTTAGCAAGTITTIGTCATAGCTAACATTATAGGTGTA 5933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGGAGGAAGATAGGGAGCAATTAAAGGAGTGGGCTGCGAGTCTCATTCA 5983
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; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-09-105-537-38 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and
FILE REFERENCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 38
LENGTH: 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38, Application US/09105537A Patent No. 6265202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6434 TAGCATATTCACGAACCCCGATGTCTTCGATATTACGAGAAGTCCTAATC
                                                                                               117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              386 hrMetPheArgGlyLeuAlaSerLeuProIleAlaPhe 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  354 AlaArgThrGlnLeuArgAlaAlaVal...AlaAlaLeuAlaArgLeuPr 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287
31 pProValHisArg.......GlyAlaHisArgValTrpTyrValS 44
                                                                                                                                                                             67 GATTTCGCGGCCGATCCGTATCCGACGTACGCGAGACTGCGTGCCGAGGG 116
                                                                                                                                                                                                                       15 AspValArgArgAspProTyrProSerTyrHisTrpLeuLeuArgHisAs
                                                                                        TCCGGCCCACCGGGTGCGCACCCCCGAGGGGGGACGAGGTGTGGCTGGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgArgAspAspValValValleuAlaGlyAlaAlaAsnArgAspPr 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              er {\tt AsnThrArgGlnLeuAspValAspValGluLeuArgGlyArgArgLeu}
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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2.216
61.055
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Gaps: 8
Percent Identity: 34.673
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1031 ATCTCGCCTTCGGCCACGCCATCCACTTCTGCATCGGCGCCCCCTTGGCC 1080
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                                                                                                                                                                                                                                                                                                                                                                                                                                            831 CGGCGCGGTGGAGGAGGTTGCGCTACGAGGGCCCGGTGGAATCCGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluAspLeuLeuAlaLeuMetLeuAspAlaHisAspArg......GlyLe 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aLeuAlaArg......GlyAlaMetAspValValAspGluLeuAlaTyrP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgLeuGluProValIleAlaGlyThrValAspAspLeuLeuArgProAl 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uMetSerArgAsnGluIleValSerThrValValThrPheIlePheThrG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heAlaAspTyrValGluArgAlaLeuAlaArgArgArgArgGluGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTCGTCTTCCCGGACGATCCCGCCCAGGCCCAGACCGCCATGGCCGAGA 580
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                                                                                                                                                 GCGCTTCCCGGACCCGCACCGCTTCGACATCCGCCGGGACACCGCCGGCC 1030
                                                                                                                                                                                                                                               GGCACGAGACCACGGTCAATCTGATCGCCAACGGCATGTACGCGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGACCTGCTCAGCGCGCTCGTGCGGACCAGCGACGACGACGGCTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAGCGGCTATCTCCCCGGCTCATCGACTCCAAGCGCGGGCAGGACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gGlyAlaSerAlaGluAspMetArgArgGlyHisAlaAlaIleAlaGluP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TrpGlyAlaValGlyArgTrpSerArgAspValGlyArgThrLeuAspAr 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTGGCGGCGCCGACGGCCGCCGATCTGATGGAGTCCCTGGCCTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCGGCTGCGCAAGCTGGTGGCCCGTGAGTTCACCATGCGCCGGGTCGAG
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                                                                                           erMetSerPheGlyAlaGlyMetArgTyrCysLeuGlySerTyrLeuAla 354
                                                                                                                                                                                            gArgTyrAspArgProAspAspPheAspIleGluArgAspProValProS
                                                                                                                                                                                                                                                                                           ArgAspAspValValValValLeuAlaGlyAlaAlaAsnArgAspProAr 321
                                                                                                                                                                                                                                                                                                                                                                                            hrArgGlnLeuAspValAsp...ValGluLeuArgGlyArgArgLeuArg 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aGlnAlaValGluGluCysLeuArgTyrAspProSerValGlnSerAsnT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCGCACCCGACCAGCTGGCCGCCCTGCGGGCCGACATGACGCTCTTGGA 830
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ArgThrGlnLeuArgAlaAlaVal...AlaAlaLeuAlaArgLeuProGl 370
                                                                                                                                                                                                                                                                                                                                                CCTACCGCTTCCCGGTCGAGCCCGTCGACCTGGACGGCACGGTCATCCCG
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seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-09-320-878-21
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US-09-724-797-36 x US-09-320-878-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-320-878-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER APPLICATION NUMBER: 60/10,880
EARLIER FILING DATE: 1998-09-22
EARLIER FILING DATE: 1998-09-22
                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-09-320-878-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 21
LENGTH: 5970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie
APPLICANT: BETLACH, Mary C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21, Application US/09320878A Patent No. 6117659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: McDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1131
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                                                                                   1422 GATTTCGCGGCCGATCCGTATCCGACGTACGCGAGACTGCGTGCCGAGGG
                                                                                                                                                                              1472 TCCGGCCCACCGGGTGCGCACCCCCGAGGGGGGACGAGGTGTGGCTGGTCG
                                                                                                                                                                                                                      31 pProValHisArg......GlyAlaHisArgValTrpTyrValS 44
                                      61 ThrGlyIleArgArgPheTrpThrAspLeuValGlyProGlyLeuLeuAl
                                                                                                                                                                                                                                                                                                                 15 AspValArgArgAspProTyrProSerTyrHisTrpLeuLeuArgHisAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGATTCGCGGGCTCAAGGCCCTGCCGATCCGCTGGCGGCGAGGA 1224
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Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1857 CGCGCCGCCTTCCGCGTCTGGACC......GACGC 1885
                                                                                                                                                                                                                                                                                                                                                                                                                2286 GCCGGTGACACGGTCCTCGTCGTCCTGGCCGACGCCCACCGCACCCCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2136 TCGCACCCGACCAGCTGGCCGCCCTGCGGGCCGACATGACGCTCTTGGA 2185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2036 GCTGACCTCCGAGGAGCTGCTCGGTATGGCCCACATCCTGCTCGTCGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1986 GAGGACCTGCTCAGCGCGCTCGTGCGGACCAGCGACGAGGACGGCTCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1657 CCCGCCTGCGCAAGCTGGTGGCCCGTGAGTTCACCATGCGCCGGGTCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 lyHisGluThrValAlaSerGlnValGlyAsnAlaValLeuSerLeuLeu 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 GluAspLeuLeuAlaLeuMetLeuAspAlaHisAspArg.....GlyLe 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 heAlaAspTyrValGluArgAlaLeuAlaArgArgArgArgGluGlyGly 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 gGlyAlaSerAlaGluAspMetArgArgGlyHisAlaAlaIleAlaGluP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158 TrpGlyAlaValGlyArgTrpSerArgAspValGlyArgThrLeuAspAr 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 aLeuAlaArg.....GlyAlaMetAspValValAspGluLeuAlaTyrP 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 ArgAspAspValValValLeuAlaGlyAlaAlaAsnArgAspProAr 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 AlaHisProAspGlnLeuAspLeuLeuArgArgArgProAspLeuLeuAl 272
370 yLeuArgLeuGlyCysAlaSerAspAlaLeuAlaTyrGlnProArgThrM 387
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                                                                                                                                                                         ATCTCGCCTTCGGCCACGGCATCCACTTCTGCATCGGCGCCCCTTGGCC
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                                                                                                                                                                                                                                                                                             GCGCTTCCCGGACCCGCACCGCTTCGACATCCGCCGGGACACCGCCGGCC
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                                                      CGGTTGGAGGCCCGGATCGCCGTCCGCGCCCTTCTCGAACGCTGCCCGGA 2485
                                                                                                             ArgThrGlnLeuArgAlaAlaVal...AlaAlaLeuAlaArgLeuProGl 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               uMetSerArgAsnGluIleValSerThrValValThrPheIlePheThrG
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APPLICANT: Schupp, Thomas
APPLICANT: Schupp, Thomas
APPLICANT: Engel, Matalie
APPLICANT: Bietenhader, Jurg
APPLICANT: Toupet, Christine
APPLICANT: Toupet, Christine
APPLICANT: Pospiech, Andreas
TITLE OF INVENTION: Staturosporin Biosynthesis Gen
FILE REFERNCE: 4-20555/A/PCT
CURRENT APPLICATION NUMBER: US/09/029,603
CURRENT FILING DATE: 1998-03-20
EARLIER APPLICATION NUMBER: PCT/EP96/03643
EARLIER APPLICATION DATE: 1996-08-19
NUMBER OF SED ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEO ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (5071)...(6085); COTHER INFORMATION: ORF US-09-029-603-4
                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-724-797-36 x US-09-029-603-4
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                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-09-029-603-4 from: 1 to: 6085
                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
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LOCATION: (4013)..(4999)
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LOCATION: (1747)..(2553)
OTHER INFORMATION: ORF
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LOCATION: (378)..(1665)
OTHER INFORMATION: ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Streptomyces longisporoflavus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: ORF
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OTHER INFORMATION: ORF
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LOCATION: (2593)..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 6085
                                                                                                                                                                    441 CCCTACCCGGTCTACCGGCGCTACCGGGAGGCCGCCCCGGTCCATCGCAC 490
                                                                        491 GGCGGCGGGCCCCGGAAAGCCTGACACCTACTACGTGTTCACCTACGACG
                    48 spValArgAlaValLeuGlyAspGluArgPheAlaArgThrGlyIleArg 64
                                                                                                                                                                                                 20 ProTyrProSerTyrHisTrpLeuLeuArgHisAspProValHisArg..
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09029603
                                                                                                                 ....GlyAlaHisArgValTrpTyrValSerArgPheAlaA 48
508.50
2.101
59.459
                                                                                                                                                                                                                                                                                                                                                                        Length: 407
Gaps: 11
Percent Identity: 36.364
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541	CGGCCGCAACGCC	84
585 585	ArgPheTrpThrAspLeuValGlyProGly7 ::: ::! cccGTGGCCTCCGGCGCACACCGGCCCCGATCCC 6	34
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635	CCGAGCACCGCGCCCTGCGGACCGTCGTCGAGAACTGGCTGG	84
8 7	<pre>lnAspGluProAspHisGlyArgLeuArgGlyValValGlyProAlaPhe 1 </pre>	03
104 735	SerProSerAlaLeuArgArgLeuGluProValIleAlaGlyThrValAs 1	20
120	AspLeuLeuArgProAlaLeuAlaArgGlyAlaMetAspValValAs	37
	AACTCCTGGACCGGCTCCGAGCACACCGCCGGCCCGATCTCGTC	34
137 835	luLeuAlaTyrProLeuAlaLeuArgAlaValLeuGlyLeuLeuGlyLeu 1 GTTCGCGGCGCCCCTCCCCGATCCTCGTCATCTGCTGGCATC	5 3 8 4
154	.ProAlaAlaAspTrpGlyAlaValGlyArgTrpSerArgAs 1	67
167	ValGlyArgThrLeuAspArgGlyAlaSerAlaGluAspMetArgAr	84
935	GCGCGGCGGCCACGGTACG	75
184 976	eAla CCAG	00 025
201 1026	yGlyGluAspLeuLeuAlaLeuMetLeuAspAl 2 ::: CCGCGACGATCTGCTCACCCTCCTCGTCCGCGC 1	17 075
217	aHisAspArgGlyLeuwetSerArgAsnGluIIIeValSerThrValV 2	33
233	ThrPheIlePheThrGlyH1sGluThrValAlaSerGlnValGlyAsn	9
	aVa Leu Parteu Leu Parteu August Augus	, ת א
7	CGCGCCCACCCTGACGTCCTCGACGAGCTGCGCAC	
0	aGlnAlaValGluGluCysLeuArgTyrAspP	ω
ו מ	GervalClascorrent and laterwal to the control of th	
1276	+ ∃ S	325
0	lyArgArgLeuArgAsgAsgAsgValValValValLeuAlaGlyAlaAl	σ
316	AsnArgAspProArgArgTyrAspArgProAspAspPheAspIleGlu	ω
1376	GCTTCCCGGCTCCCGACGTGCT	425
333	rgAspProValProSerMetSerPheGlyAlaGlyMetArgTyrCYsLeu 3	49

alignment_block: US-09-724-797-36 x US-09-428-517-1

Align seg 1/1 to: US-09-428-517-1 from: 1

to: 50937

4 AspAlaValThrAlaPheAspProThrAspAlaAspValArgArgAspPr 20

65 gPheTrpThrAspLeuValGlyProGlyLeuLeu...AlaGluIleValG 81

46621 GCCTGCCCTACGGCGAGGGCACGGCCTGGCTGGTCACCCGCATGTCCGAC 46670

36GlyAlaHisArgValTrpTyrValSerArgPheAlaAsp 48

46571 CGACCCGCACTACGCCGAACTCCGCCGCGACGAACCCGTCTCCAGGGTGC 46620

20 oTyrProSerTyrHisTrpLeuLeuArgHisAspProValHisArg.... 35

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47273 GACCGAGCGCAAGCGCTACGAGTCGCTGGTCGCCGACCCGGCCCTCGTGC 47322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47223 GGCCACGAGACGTCGGTCAACCAGATCACCAACCTCGTCCACCTCCTGCT 47272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47173 ACCTGACCAAGGGCGAGATCGTCAACATGGGGGTGAGCCTGCTCATCGCG 47222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47073 GACTTCATGGTCTACATGGACGGCCTGGTCGCCAGCGCCGCGACGCCCC 47122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47035
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                                                                                                      47523 CCGCACATAGCGTTCGGGCACGGAGCGCACCACTGCATCGGCGCCCCAACT 47572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47373 AGCTTCGTCCGCGTGGCCACCGAGGACGTGGAGCTGAGCACCGTGACCGT 47422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46859 TGTCCGCTCCCTCGTCGACTCCCTGCTCGACGACATGGTGGCGCACGGTT 46908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47323 CCGCGGCGGTGGAGGAGGTGCTGCGGTACACACCGCTGGTGTCCGCCGGC 47371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 ..argGlyAlaSerAlaGluAspMetArgArgGlyHisAlaAlaIleAla 189
||| ::::::||||| ::::||
7035 CCCGGCTCACCGCGGGGATACAGCGG......GTCCAGCAG 47072
                                                                                                                                                                                                                                                                                                                                                                                                                                303 uArgArgAspAspValValValValLeuAlaGlyAlaAlaAsnArgAspP 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 laGlnAlaValGluGluCysLeuArgTyrAspProSerValGlnSerAsn 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114 lileAlaGlyThrValAspAspLeuLeuArgProAlaLeuAlaArgGlyA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 uAlaHisProAspGlnLeuAspLeuLeuArgArgArgProAspLeuLeuA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 euMetSerArgAsnGluIleValSerThrValValThrPheIlePheThr 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206 yGlyGluAspLeuLeu...AlaLeuMetLeuAspAlaHisAspArgGlyL 222
353 uAlaArgThrGlnLeuArgAlaAlaValAlaAlaLeuAla...ArgLeuP 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 lyAspIleIleLeuPheGlnAspGluProAspHisGlyArgLeuArgGly 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGACGGCGTCCTCGCCCAGGACCCGCCGGACCACCCCGGCTGCGGCGG 46808
                                                                                                                                                                                                                                              AGGAGGTCTTCGACCACGCCGACGACCTGGACTTCCACCGTGAGCGCAAC 47521
                                                                                                                                                                                                                                                                                                                  roArgArgTyrAspArgProAspAspPheAspIleGluArgAspProVal 336
                                                                                                                                                                                                                                                                                                                                                                                      GCGGGCCGGGGAGCCCTGCGTCGTCCACTTCGCGTCGGCCAACCGGGACG 47472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACCGAGGACCTGGCGCGCCCTCGCCCTCGCCACCGACAACGACGACC 47172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluPheAlaAspTyrValGluArgAlaLeuAlaArgArgArgArgGluGl 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValLeuGlyLeuGlyLeuProAlaAlaAspTrpGlyAlaValGlyAr 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               la...MetAspValValAspGluLeuAlaTyrProLeuAlaLeuArgAla 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValValGlyProAlaPheSerProSerAlaLeuArgArgLeuGluProVa 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thr.....ArgGlnLeuAspValAspValGluLeuArgGlyArgArgLe 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyHisGluThrValAlaSerGlnValGlyAsnAlaValLeuSerLeuLe 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....ACCGATCCCGCCACCCCCGGATGTTCCCCACCCCGAGC 46758
                                                                                                                                                                      ProSerMetSerPheGlyAlaGlyMetArgTyrCysLeuGlySerTyrLe 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....CGCGACCTGTTCCGGACCTTCTCCGACGCCATGCTCTCCTCGA 47034
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NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
SEQ ID NO:17:
LENGTH: 1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block: US-09-724-797-36 \times 5212296-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5212296-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.; TEPPERMAN, JAMES M.
TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
;Patent No. 5212296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/1/ina/backfiles1.seq:5212296-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; CYTOCHROMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: 5212296-17 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47723 CGCCCGGCCGCCCGCCGGG 47741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386 ThrMetPheArgGlyLeuAlaSer.....LeuProIl 396
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113 ProValIleAlaGlyThrValAspAspLeuLeu...ArgProAlaLeuAl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                 176 ACGTCCGCGCGCTCCTCGGCGACCCGCGCTTCAGCGCCGACGCCCACCGC 225
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                                                                                                                                                                                                                                                                                                            226 ACCGGCTTCCCCTTCCTGACCGCCGGCGC.....CGCGAGATCATCGG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 GGCCACCCTCTGGGACGGCTCCTCCTGCTGGCTGGTGACGCGCCATCAGG 175
                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 spValArgAlaValLeuGlyAspGluArgPheAlaArgThrGlyIleArg 64
                                                                                                                                                                                                                                                                                                                                                                      65 ArgPheTrpThrAspLeuValGlyProGlyLeuLeuAlaGluIleValGl 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 gGly.....AlaHisArgValTrpTyrValSerArgPheAlaA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 GACCCCGCGCCCGACGTCACCGAGGCGGCCCGCACCGAACCGGTCACCCG
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                                                                                                                                                                                                                                                  y.....AspIleIleLeuPheGlnAspGluProAspHisGlyArgLeuA 96
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                                                                                                                                          rgGlyValValGlyProAlaPheSerProSerAlaLeuArgArgLeuGlu 112
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1.924
60.668
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Gaps: 10
Percent Identity: 34.447
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seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-103-840A-2
seq_documentation_block:
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APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, OWEN R.
APPLICANT: WHITE, OWEN R.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DAA SEQUENCES FOR STRAIN
TITLE OF INVENTION: DUA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 198-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA ; OTHER INFORMATION: CDC 1551 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence ; OTHER INFORMATION: represent a, t, c or g US-09-103-840A-2 alignment_block: US-09-724-797-36 x US-09-103-840A-2/rev alignment_scores: Align seg 1/1 to reverse of: US-09-103-840A-2 Percent Similarity: GENERAL INFORMATION: Sequence 2, Application US/09103840A Patent No. 6294328 2540999AACCACGACACGTTGTCCAGCGCCCGTGGGGTCACCTTCTCACGGGGGTG 2540950 2541049GCGACGTCTACATTTTGAGCCGATACGCCGACGTCCGCGAGGCTGCGCGT 2541000 2541099GCATTATCGAGAGCTGTTGGCCGGCGAGCGGGTGCAGTACAACCCCAAGC 2541149CTCACCGACTTTGACCCGTTTCGATCCCGCGATTGCCGCTGATCCTTACCC 2540888CCAGGTATGGCGCGTGGCGCGTTGGAGACGTGGCGCCCGATGGTCGACCA 2540839 2540930.....rccgarccgccggcgcacacccggargcgcaagcaactggca 2540889 2540788TCGTCTCCACCGTGGCCGCACCGATGCCGATGCGCGCTATCACCAGTGTG 2540838GCTTGCCCGAGAACTGGTCGGCGGGTTACTGACCCAGACGCCCGCGGACG 2540949GCTGCCGTTTCTGCCGACG........... ORGANISM: Mycobacterium tuberculosis FEATURE: 101 ProAlaPheSerProSerAlaLeuArgArgLeuGluProValIleAlaGl 117 134 alValAspGluLeuAlaTyrProLeuAlaLeuArgAlaValLeuGlyLeu 67 53 LeuGlyAspGluArgPheAlaArgThrGlyIle.....ArgArgPheTr 67 39 22 oSerTyrHisTrpLeuLeuArgHisAspProValHisArgGlyAlaHisA 84 leLeuPheGlnAspGluProAspHisGlyArgLeuArgGlyValValGly 100 6 ValThrAlaPheAspProThrAspAlaAspValArgArgAspProTyrPr rg...ValTrpTyrValSerArgPheAlaAspValArg.....AlaVal 52 yThrValAspAspLeuLeuArgProAlaLeuAlaArgGlyAlaMetAspV 134 pThrAspLeuValGlyProGlyLeuLeuAlaGluIleValGlyAspIleI 84 Quality: Ratio: 446.00 1.890 57.005 Gaps: Percent Identity: FOR STRAIN ANALYSIS IN MYCOBACTERIUM from: 1 414 11 31.401 to: 4403765 2540931 2541050 2541100 2540739 2540789

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seq_documentation_block:
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; Patent No. 6294328
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GENERAL INFORMATION:
APPLICANT: FLEISCHANN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                2540030AACCTTCGCGGCTTGACCCGGTTACGGGTCGCCGTTACCCCC 2539989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2540063......GTGGTCGAGCCGCCGACGTGGACGACAAACGCC 2540031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2540097GCGCGAGATCGTCGCCAATATCGACCGAATAGAG.......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2540347TCCGCTTTATATCGCCAATCCAAAACATCTGCCGCACAACGCGCGTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2540397ACTCCTTGCGCAGCAACCAGACCTGATCCCGTCGGCGATCGAGGAGCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2540447ATGATTAGCACATTGTTTCTGACGCTGGCCGACTATCCAGATCAGCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2540497TCTTCTTCGCGGTGTTGCTGCTGGTTGCGGGCTATGAGAGCACTGCTCAT 2540448
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; ORGANISM: Mycobacterium tuberculosis; OTHER INFORMATION: H37Rv US-09-103-840A-1
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US-09-724-797-36 x US-09-103-840A-1/rev
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    Quality:
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Percent Similarity:
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LENGTH: 4411529
                                                             2543476..ATTTCGCTTGTGCAGGGCTTTGCCGGATTCCGGCGATTGCGTGCACTC
                                                                                                                                                                           2543519GGGGTACGGATCACCGACGTTGCCTTGTCAGCCTCCGGGTTG.....
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                                                                                                           184 lyHisAlaAlaIleAlaGluPheAlaAspTyrValGlu...ArgAlaLeu 199
                                                                                                                                                                                                                                                                                                                                                    151 LeuGlyLeuProAlaAlaAspTrpGlyAlaValGlyArgTrpSerArgAs 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 alValAspGluLeuAlaTyrProLeuAlaLeuArgAlaValLeuGlyLeu 150
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200 AlaArgArgArgGluGlyGly......GluAspLeuLeuAlaLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 LeuGlyAspGluArgPheAlaArgThrGlyIle.....ArgArgPheTr 67
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Gaps: 11
Percent Identity: 31.401
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seq_documentation_block:
;Patent No. 5212296
; Patent No. 5212296
; APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNI;
;J.; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.; TEPPERMAN, JAMES M.
;TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/ina/backfiles1.seq:5212296-8
                            SEQ ID NO:8:
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 ... PheArgGlyLeuAlaSerLeuProIleAlaPheThrPro
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                                                                                      APPLICATION NUMBER: 464,499 FILING DATE: 12-JAN-1990 APPLICATION NUMBER: 405,605
LENGTH: 1998
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alignment_block:
US-09-724-797-36 x 5212296-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 aGluAspMetArgArgGlyHisAlaAlaIleAlaGluPheAlaAspTyrV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 ProVallleAlaGlyThrValAspAspLeuLeu...ArgProAlaLeuAl 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 GGCCACCCTCTGGGACGGCTCCTCCTGCTGGCTGGTGACGCGCCATCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 GACCCCGCGCCCGACGTCACCGAGGCGGCCCGCACCGAACCGGTCACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48 spValArgAlaValLeuGlyAspGluArgPheAlaArgThrGlyIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 AspProTyrProSerTyrHisTrpLeuLeuArgHisAspProValHisAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 gGly.....AlaHisArgValTrpTyrValSerArgPheAlaA
LeuAspLeuLeuArgArgProAspLeuLeuAlaGlnAlaValGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regrearcrectecrecrecectaceaegaccacecerrete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aArgGlyAlaMetAspValValAspGluLeuAlaTyrProLeuAlaLeuA 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCAACCCGACCTTCCTGCGCATGGACGACCCGGAGCACGCCCGACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCGGCTTCCCTGACCGCCGGCGGC.....CGCGAGATCATCGG
                                                                                                                                                                                             eValSerThrValValThrPheIlePheThrGlyHis...GluThrValA
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                                                                                                                                                                                                                                                                                                                             TCGCCCGG...CTCGCCCGGACCAAGCGGGAGGGGCGGACGACGACGCCATC
                                                                                                                                                                                                                                                                                                                                                      alGluArgAlaLeuAlaArgArgArgArgGluGlyGlyGluAspLeuLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rgAlaValLeuGlyLeuGlyLeuProAlaAlaAspTrpGlyAlaVal 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGCACCTCCGCCGACCTGGTCACCGAGTTCGCGCTGCCGCTGCCGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCGAGGTGCAGCGCCTCGCCGACGACCTGGTCGACCGGATGACCACCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACGTCCGCGCGTCCTCGGCGACCCGCGCTTCAGCGCCGACGCCCACCGC
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                                                                                                                                                                                                                                                                                  AlaLeuMetLeuAspAlaHisAspArgGlyLeuMetSerArgAsnGluIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rgGlyValValGlyProAlaPheSerProSerAlaLeuArgArgLeuGlu 112
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;Patent NO. 5212296
; APPLICANT: DEAN, CAROLINE;HARDER, PATRICIA A.;LETO, KENNETH
;J.; O'KEEFE, DANIEL P.;OMER, CHARLES A.;ROMESSER, JAMES A.;TEPPERMAN, JAMES M.
;TEPPERMAN, JAMES M.
;TEPPERMAN, JAMES M.
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                                                                                                                                                                  Align seg 1/1 to: 5212296-16 from: 1
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APPLICATION NUMBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1284 ATCGCCATCGAAACGCTGCTGCGCCCGCCTGCCGGACCTGCGGCTGGCCGT 1333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1134 CTGTGCATGATCAGCTCCGCCAACCGGGGACGCCGAGGTGTTCCCCCGGCGG 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1334 GCCCCACGAGGAGATCCCGTTCCGCGGCGACATGGCGATCTACGGGGTCC 1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1184 CGACGACCTCGACGTGGCCCGCGACGCCGCCGCCACGTGGCCTTCGGCT 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1034 GCTGCTGCGCTACCTGACGATCGTGCACAACGGCGTTCCCCGGATCGCCA 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             375 sAlaSerAspAlaLeuAlaTyrGlnProArgThrMetPheArgGlyLeuA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 AlaAlaVa1...AlaAlaLeuAlaArgLeuProGlyLeuArgLeuGlyCy 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 oAspAspPheAspIleGluArgAspProValProSerMetSerPheGlyA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 ValValLeuAlaGiyAlaAlaAsnArgAspProArgArgTyrAspArgPr 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294 al...AspValGluLeuArgGlyArgArgLeuArgArgAspAspValVal 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 laSerLeuProIleAlaPheThrProGly 401
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                           17
                                                                                                ENGTH: 1221
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1.625
61.045
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Gaps: 13
Percent Identity: 30.166
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29 101	rgHisSpProValHisArgGlyAlaHisArg	39 150
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3 1 1	01.085************************************	, ,
377	Interest	
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230 706	SerThrValValThrPheIlePheThrGlyHisGluThrValAlaSerGl ::::: ::::::::: :::	246 755
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NUMBER OF SEQUENCES: 19
CURRENT APPLICATION LOBATA:
APPLICATION UNBER: US/07/569,781
FILING DATE: 23-AUG-1990
PRIOR APPLICATION UNBER: 464,499
FILING DATE: 12-JAN-1990
APPLICATION NUMBER: 405,605
APPLICATION NUMBER: 405,605
FILING DATE: 11-SEP-1989
SEQ ID NO:5:
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    Percent Similarity:
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5212296-5
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US-09-724-797-36 x 5212296-5
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patent No. 5212296
APPLICANT: DEAN, CAROLINE; HARDER, PATRICIA A.; LETO, KENNETH
J.; O'KEEFE, DANIEL P.; OMER, CHARLES A.; ROMESSER, JAMES A.
TEPDERMAN, JAMES M.
TITLE OF INVENTION: EXPRESSION OF HERBICIDE METABOLIZING
CYTOCHROMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/ina/backfiles1.seq:5212296-5
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1206 CCCGGTCACCTGG 1218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1106 TCAACGCCTCATGGACCGCGTCCCGACGCTGCGACTGGCCGTCCCCGTC 1155
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278 GCGTGGGTGACCAAGCACGAGGCCGCGCAAACTGCTCGGCGACCC 327
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                                                                                                                                                                                                                                                                               128 ATGACCGATACCGCCACGACGCCCCAGACCGCACGGACGCCACCGCCTTCCC 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 euAlaGlyAlaAlaAsnArgAsgProArgArgTyrAspArgProAspAsp 328 :: ::: |||||||||
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                                                                                                                                                                                                                                                                                                                       2 LeuValAspAlaValThrAlaPheAspProThrAspAlaAspVal.... 16
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Percent Identity:
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: 13
: 30.166
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345 1182	PheAspIleGluArgAspProValProSerMetSerPheGlyAlaGlyMe :::: ::: ::: :: CTCGACATCCACCGCTCCGCGCGCGCACCACCTCGGCTTCGGCCTTCGGCGT	329 1133
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                                                                                                                                                                 US-08-102-863-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-102-863-10
                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/08102863 Patent No. 5466590 GENERAL INFORMATION:
                                                                                                                                                                                                                                       TELEFAX: 302-892-703-10:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1735-5086 Pairs
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: CR-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-7342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 alAlaAlaLeuAla...ArgLeuProGlyLeuArgLeuGlyCysAlaSer 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 uProIleAlaPhe 398
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: LUU,
CITY: WILMINGTON
CTTY: CTTAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                   STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: E. I.
ADDRESSEE: AND CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAACGCCCTCATGGACCGCGTCCCGACGCTGCGACTGGCCGTCCCCGTC
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                                                                         Ratio:
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1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                     410.00
1.760
54.439
                                                                                                                                                                              DNA (genomic)
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EXPRESSION OF P450SOY
AND FERREDOXIN-SOY IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREPTOMYCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/102,863
                                                        Percent
                                                                                                                                                                                                                                                                                                                                                                  CR-9000
                                       Identity: 29.439
                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1282
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Align seg 1/1 to: US-08-102-863-10 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 GACCCCACC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 laLeuArgArgLeuGluProValIleAlaGlyThrValAspAspLeuLeu 123
                                                                                                                                                                                                             222 LeuMetSerArgAsnGluIleValSerThrValValThrPheIlePheTh 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 alHisArgGly......AlaHisArg 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 .....TyrHisTrpLeuLeuArgHisAspProV 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 AspProThrAspAlaAspValArgArgAspProTyrProSer......
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                                                                                                                                                                    CCGGTCGACCGCGAACAGCTGGTCGCCTTCGCCGTCATCCTGCTCATCGC
                                                                                                                                                                                                                                                                   CGAACTCGAGGAGTACCTGGGCGCGCTGATCGACCGCAAGAGGGGCGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt aGluPheAlaAspTyrValGluArgAlaLeuAlaArgArgArgGluG}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                laAspTrpGlyAlaValGlyArgTrpSerArgAspValGlyArgThrLeu 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGCCGGTGCCGTCGATGGTGATCTGTGCTCTGCTCGGCGTGCCCTACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GACGCGATGGAGCGACAAGGGCCCCCGGCCGAACTGGTGAGCGCGTTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGATCGGCGCCTCCGCCGCGTATCCAGGAGACCGTGGACCGGCTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyLeuLeuAlaGluIleValGlyAspIleIleLeuPheGlnAspGluPr 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTTCGCCGGCGCAGCGGCGCGCGTC......483
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                    euAlaHisProAspGlnLeuAspLeuLeuArgArgProAspLeuLeu 271
                                                                                                                   rGlyHisGluThrValAlaSerGlnValGlyAsnAlaValLeuSerLeuL 255
                                                                                                                                                                                                                                                                                                                  lyGlyGluAspLeuLeu...AlaLeuMetLeuAspAlaHisAspArgGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGAGCACAACACCCAGCGCAGGATGCTCATCCCGACCTTCTCGGTGAAGC
                                                                     CGGGCACGAGACGACGGCAACATGATCTCGCTCGGCACGTTCACGCTGC
....TCCCCGGCCCCCGCGACGTCCTT
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seq_name: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:PCT-US92-10885-10
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: GALLEGOS, R. THOMAS
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: CR-9000-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-7342
TELEPHONE: 302-892-7949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1735 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application PC/TUS9210885 GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 nThrArgGlnLeuAspValAspValGluLeuArgGlyArgArgLeuArgA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 AlaGlnAlaValGluGluCysLeuArgTyrAspProSerValGlnSerAs 288
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                                                                                                                                                                                                                                                                                                                                                                        STATE: DELAWARE
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 1.0 MB
                                                                                                                                                                                                                                                COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System,
OPERATING SYSTEM: Macintosh System,
SOFTWARE: Microsoft Word, 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10885
FILLING DATE: 19921216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCCAGGGCCTCCTCGACCTGCCCGTGGCCTGG 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGCCGAGCTGGACATCGCGATGCGCACCCTGTTCGAGCGGCTTCCCGGG 1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuArgLeuGlyCysAlaSerAspAlaLeuAlaTyrGlnProArgThrMe 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGGGGGAGGGCGTGGTCTTCTCGACCTCGCTGATCAACCGCGACGCCGAC 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SARIASLANI, SIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXPRESSION OF P450SOY AND FERREDOXIN-SOY IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREPTOMYCES
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                                                                                                                                                                                                                                                                                                                                        6.0
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189 aGluPheAlaAspTyrValGluArgAlaLeuAlaArgArgArgArgGluG 206 ::: :: ::: 786 CGAACTCGAGGAGTACCTGGGCGGCGCTGATCGACCGCAAGAGGGCGGAGC 835	
173 AspArgGlyAlaSerAlaGluAspMetArgArgGlyHisAlaAlaIleAl 189 745 CTGCGCGGCCCGGGAGCCGACGATGTGAACAGGGCCCGCGA 785	
156 laAspTrpGlyAlaValGlyArgTrpSerArgAspValGlyArgThrLeu 172	
139 aTyrProLeuAlaLeuArgAlaValLeuGlyLeuLeuGlyLeuProAlaA 156	
124 ArgProAlaLeuAlaArgGlyAlaMetAspValValAspGluLeuAl 139 :::: :::::::::::::::::::::::::::::::	
107 laLeuArgArgLeuGluProVallleAlaGlyThrValAspAspLeuLeu 123 ::: :::	
90 OASPHISGIYATGLEUATGGIYValValGIYPTOAlaPheSerPTOSETA 107 ::: ::: ::: ::: ::: ::: 507 CGAGCACAACAGCCAGCGCAGGATGCTCATCCCGACCTTCTCGGTGAAGC 556	
74 GlyLeuLeuAlaGluIleValGlyAspIleIleLeuPheGlnAspGluPr 90	
57 rgPheAlaArgThrGlyIleArgArgPheTrpThrAspLeuValGlyPro 73 :: 455 GGTTCGCCGGCGCGCAGCGCGCGCCGCGTC	
56	
40 ValTrpTyrValSerArgPheAlaAspValArgAlaValLeuGlyAsp 55	
33 alhisargGlyAlahisarg 39 :::::::: ::::::::::::::::::::::::::	
24TyrHisTrpLeuLeuArgHisAspProV 33	
10 AspProThrAspAlaAspValArgArgAspProTyrProSer 23	
Align seg 1/1 to: PCT-US92-10885-10 from: 1 to: 1735	
alignment_block: US-09-724-797-36 x PCT-US92-10885-10	
alignment_scores: Quality: 410.00 Length: 428 Ratio: 1.760 Gaps: 10 Percent Similarity: 54.439 Percent Identity: 29.439	
; TYPE: NUCLEIC ACID ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) PCT-US92-10885-10	

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kosan Biosciences, Inc.
APPLICANT: Matz, Leonard
APPLICANT: Kosa, Chaitan
APPLICANT: Khosla, Chaitan
APPLICANT: Tang, Li
APPLICANT: Tang, Li
APPLICANT: Teleman, Rainer
TITLE OF INVENTION: Recombinant Methods and Materials for Producing
TITLE OF INVENTION: Epothilone and Epothilone Derivatives
FILE REFERENCE: 30062-20031.00
CURRENT APPLICATION NUMBER: US 60/130,560
PRIOR APPLICATION NUMBER: US 60/130,560
PRIOR APPLICATION NUMBER: US 60/122,620
PRIOR APPLICATION NUMBER: US 60/123,630
PRIOR FILING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: US 60/119,386
PRIOR APPLICATION NUMBER: US 60/119,401
PRIOR APPLICATION NUMBER: US 60/119,401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 rGlyHisGluThrValAlaSerGlnValGlyAsnAlaValLeuSerLeuL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222 LeuMetSerArgAsnGluIleValSerThrValValThrPheIlePheTh 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206 lyGlyGluAspLeuLeu...AlaLeuMetLeuAspAlaHisAspArgGly 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tPheArgGlyLeuAlaSerLeuProIleAlaPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCAGGCTCGCCGTACCCGCGCACGAGATCCGTCACAAGCCGGGGGACAC 1385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuArgLeuGlyCysAlaSerAspAlaLeuAlaTyrGlnProArgThrMe 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGCCGAGCTGGACATCGCGATGCGCACCCTGTTCGAGCGGCTTCCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCGCCTTCGGCTTCGGAGTCCACCAGTGCCTGGGCCAGAACCTGGCCC 1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rMetSerPheGlyAlaGlyMetArgTyrCysLeuGlySerTyrLeuAlaA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGTTCCCCCGGGCCGAGACACTCGACTGGGACCGCCCCGCCCATCA 1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgTyrAspArgProAspAspPheAspIleGluArgAspProValProSe
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; ORGANISM: Artificial Sequence; FEATURE:
; OTHER IMFORMATION: Synthetic US-09-443-501A-2
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SOFTWARE: FastSEQ for
SEQ ID NO 2
LENGTH: 71989
57399 GAGCGGCAGGAACCCGCTCGAAAATGACGTCTTGACGATGCTGCTTCA 57448
                                                                                                         57349 TGGTCGCGTCCGTCACCGAGGGGCTCGCGCGCTCCATGGCGTCCTCGAT 57398
                                                                                                                                                                                                                        57299 CGCGCTCGGCGTGGGTTTGGTGCCCCGGGTCGATGAGGAGACCAAGACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         57199 ATTACGCGGAGGGAATCCCGATGCGTGCGATCAGCGCTCTGTTGAAGGTT 57248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57149 CCAGCTCGATGCTCGCTCCGGACAAGAGGAGTTCGACGTTGTGCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56905 GGGTCCTCACCCGATACCACGACGTGTCCGCGTGTTCCGCGAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56855 GCGCCTGAGAGAGGCAACCCCCATCTTCTACTGGGATGAAGGCCGCTCCT 56904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57099 ACGTCACGCGATCGACCTGCTGCGCGCGAAATACAGCGCACCGTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56999 GTCGGCCATTCCCGAGCTCAGCGATATGAAGAAGTACGGATTGTTCGGGC 57048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 SerProSerAlaLeuArgArgLeuGluProVallleAlaGlyThrValAs 120
                                                                                                                                                                                                                                                                            170 gThrLeuAspArgGlyAlaSerAla.....GluAspMetArgArgG 184
                                                                                                                                                                                                                                                                                                                                                                                            154 ProAlaAlaAspTrpGlyAlaValGlyArgTrpSerArgAspValGlyAr 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 pAspLeuLeuArgProAlaLeuAlaArgGlyAlaMetAspValValAspG 137
                                              201 ArgArgArgGluGlyGlyGlu...AspLeuLeuAlaLeuMetLeuAs
                                                                                                                                                             184 lyHisAlaAlaIleAlaGluPheAlaAspTyrValGluArgAlaLeuAla 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 PheAlaArgThrGlyIleArgArgPheTrpThrAspLeuValGlyProG1 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41 rpTyrValSerArgPheAlaAspValArgAlaValLeuGlyAspGluArg 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 yLeuLeuAlaGluIleValGlyAspIleIle.....LeuPheGlnA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 sTrpLeuLeuArgHisAspProVal...HisArgGlyAlaHisArgValT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 PheAspProThrAspAlaAspValArgArgAspProTyrProSerTyrHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spGluPro...AspHisGlyArgLeuArgGlyValValGlyProAlaPhe 103
||| |||||||:::||| :::||| :::|||:::|||
                                                                                                                                                                                                                                                                                                                                       CCGGCCGAGTGTGACGAGAAGTTCCGTCGCTTCGGCTCGGCGACTGCGCG
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Gaps: 11
Percent Identity: 31.188
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57449 GGCCGAGGCCGACGCAGCAGGCTGAGCACGAAGGAGCTGGTCGCGCTCG 57498
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                                                                                                                                                                                                                                                                57946 TTGGATACCACCCC.....GCGTTCCGGAACATCGAATCACTCAACGTC 57989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57899 CATCTTCCGTAGGTTCCCCGAGATGAAGCTGAAA...GAAACTCCCGTGT 57945
57990 ATCTTGAAGCCC 58001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 yAlaAlaAsnArgAspProArgArgTyrAspArgProAspAspPheAspI 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 spProSerValGlnSerAsnThr...ArgGlnLeuAspValAspValGlu 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 alValThrPheIlePheThrGlyHisGluThrValAlaSerGlnValGly 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 pAlaHis...AspArgGlyLeuMetSerArgAsnGluIleValSerThrV 232 :|||::: ||| ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || ::: || 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                                                                                                                                                                                                                                                                                                                                                                                  380 euAlaTyrGlnProArgThrMetPheArgGlyLeuAlaSerLeuProIle 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 aLeu...AlaArgLeuProGlyLeuArgLeuGlyCysAlaSerAspAlaL 380 :::: ||||:::||| ::::::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 CysLeuGlySerTyrLeuAlaArgThrGlnLeuArgAlaAlaValAlaAl 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 leGluArgAspProValProSerMetSerPheGlyAlaGlyMetArgTyr 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 LeuArgGlyArgArgLeuArgArgAspAspValValValLeuAlaGl 314
                                                                                                                                397 AlaPheThrPro 400
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gb_est2:BG208878
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gb_htc:AK007863
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gb_est2:BG206682
gb_est2:BG182832
gb_est1:AI323114
gb_est2:BG195942
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Query: US-09-724-797-36
Query length: 402
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gb_htc:BC020267
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Database length: -1841457050
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I AAGB8024 uc72b04.yl Sugano mous

I AL530226 ui90e12.yl Sugano mous

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2 BC001776 Homo sapiens, clone I

I BC002027 Homo sapiens, clone I

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I BC204536 RST23942 Athersys RAGE

I BG182832 RST16193 Athersys RAGE

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I BG195942 RST15072 Athersys RAGE

I BG195942 RST18728 Athersys RAGE

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I BG195944 RST15072 Athersys RAGE

I BG195947 RST2829 Athersys RAGE

I BG195947 RST2829 Athersys RAGE

I BG19734 RST16556 Athersys RAGE

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I BG19489 RST136271 unpublished

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Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Physical and Chemical Research (RIKEN), Laboratory Exploration Research Group, RIKEN Gemomic Sciences
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gb_est2:BG185434
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Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

E 5 (bases 1 to 3004)

S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Haraoka, T., Hori, F., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Koya, S., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Schrimi, L., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Saito, R., Sahibata, Y., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Szuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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e RIKEN Genome Exploration Research Group Phase II Team and
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17 HNC5-1-F9 R HNC (H)
15 RST19748 Athersys |
15 RST24484 Athersys |
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Center (GSC), Institute of for Genome

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Ratio: 1.063
Percent Similarity: 47.631
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1476
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                                                                                                                                                                                                                                                                                                                                                     CTGTCCCCCACATTCACCAGTGGAAAACTCAAGGAGATGTTCCCTGTCAT 1475
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                                                                                           eAlaGlyThrValAspAspLeu.....LeuArgProAlaLeuAlaA 129
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Gaps: 13
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333	pArgProAspAspPheAspIleGluArg ::: ::: ::: ::: ::: :::	324 2260
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307 2209	InLeuAspValAspValGluLeuArgGlyArgArgLeuArgArgAspAsp ::: 	291 2160
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274 2109	ArgProAspLeuLeuAlaGlnAl	267 2060
266 2059	AspGlnLeuAspLeuLeuArgArg	259 2010
258 2009	rValAlaSerGlnValGlyAsnAlaValLeuSerLeuLeuAlaHisPro.	242 1960
242 1959	AsnGluIlevalSerThrValValThrPheIlePheThrGlyHisGluTh	226 1910
225 1909	PAlaHisAspArgGlyLeu.MetSerArg :::: :::::: TTCTCATAATTATTCTCAAAGACAAAGTCTCCTCATAAAGCCCTTTCTGAC	216 1860
216 1859	ArgargGluGlyGlyGluAspLeuLeuAlaLeuMetLeuAs .:::::::::: ::: :::: CTGGATTCTAAGCAGAAGCACCGAGTGGATTTTCTTCAGCTGATGATGAA	203 1810
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162 1559	AlaValLeuGlyLeuLeuGlyLeuProAlaAlaAspTrpGlyAlaValGl GATGTGTTAGG	146 1549

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FEATURES
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                                              alignment_block:
US-09-724-797-36 x AA986024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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AA986024
                                                                                                                                                                                                                                                                                        Institute of Medical Science). Custom primers sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG primer CGACCTGAAGCTGCAGCACA."

a 178 c 157 g 202 t 3 others
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/sex="female"
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/strain="C57BL"
                                                                                                                      187.00
1.700
57.592
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/clone="IMAGE:1431151"
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to:
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AUTHORS
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LOCUS AI530226
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                                                             1 (bases 1 to 762)

1 (bases 1 to 762)

1 (bases 1 to 762)

Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,

Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,

Waterston,R. and Wilson,R.

Waterston,R. and Wilson,R.
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                              Mus musculus
                                                Unpublished (1999)
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     306
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GTGATGGAGATGGAATACCTGGATATGGTGCTTAATGAAACCCTCAGATT
                                                                                                                                                spGlnLeuAsp.....LeuLeuArgArgArgPro.....
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                                                                                                                                                                                                                                                                                                         ATTATCTTTATTTTTGCTGGGTATGAAACCACCAGTAGCACACTTTCCTT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATTTGTGGACAGAATGAAGGAAAGCCGCCTGGATTCTAAGCAGAAGCA 55
                                             .....AspLeuLeuAlaGlnAlaValGluGluCysLeuArgTy 281
                                                                                                   ATGAGATCGATGAGGCTCTGCCCAACAAGGCACCTCCCACGTATGATACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Note-"Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments of 1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing 5' end primer CTTCTCTALABACTGCG.
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1.533
57.143
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/clone_lib="Sugano mouse liver mlia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
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355
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REFERENCE
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LOCUS BC001776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 TCAATGGTGTGTATATCCCCCAAAGGGTCAACAGTGATGATTCCATCTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 euArgGlyArgArgLeuArgArgAspAspValValValValLeuAlaGly 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 rAspProSerValGlnSerAsnThrArgGlnLeuAspValAspValGluL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrGlnLeuArgAlaAlaValAlaAlaLeu 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCCCTTTGNGAATGGACCCAGGAACTGCCTTGGCATGAGGTTTGCTCTC 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAAAGGTTCAGCAAGGAGAACAAGGGCAGCATTGATCCTTATGTATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eGluArg......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGAATATGANACTTGCTCTCACTANCATT 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               etSerPheGlyAlaGlyMetArgTyrCysLeuGlySerTyrLeuAlaArg 355
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                Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 6 Row: h Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13904864
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hislao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2492 bp mRNA linear HTC 12-Homo sapiens, Similar to cytochrome P450, subfamily XXVIIB (25-hydroxyritamin D-1-alpha-hydroxylase), polypeptide 1, c IMAGE: 3354171, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (23-JAN-2001) National Institutes of Health, Mammalian Submitted (03-JAN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg, k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                info@bcgsc.bc.ca
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Location/Qualifiers
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source

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alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
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US-09-724-797-36 x BC001776
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ORIGIN
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153 uProAlaAlaAspTrpGlyAlaValGlyArgTrpSerArgAspValGlyA 170
                                                                               141 ProLeuAlaLeuArgAlaValLeuGly.....LeuLeuGlyLe 153
                                                                                                                          665 GGCAGGCGTCGGGGGGCGCCTACCAGAGCCTCCCGGAACCCTGACGGCGC 714
                                                                                                                                                                                                          615 GGGGGAATTTTACAAGTTCGGACTGGAAGGTGAGTCCCAGGACAGAGCTG
                                                                                                                                                                                                                                                 524 CCCTGAACAACGTAGTCTGCGACCTTGTGCGGCGTCTGAGGCGCCCAGCGG 573
                                                                                                                                                                                                                                                                                                                                                                                                      474 CCTGGCCCCGCTCCTCCGGCCTCAAGCGGCCGCCCGCTACGCCGGAA 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 GGGACCCCGGCCCGAGCGCTGCAGCTTCTCGCCCTGGACGGAGCACCGCC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307 ACCGTGTACGTGGCTGCCCCTGCACTCGTCGAGGAGCTGCTGCGACAGGA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 ACTTCGGGCCG.....GTGTGGCTAGCCAGC...TTTGGGACAGTGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 AspIleIleLeuPheGlnAspGluProAspHisGlyArgLeuArgGlyVa 98
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                                        CCCCTCCCGACAAGGCATCGCCGCGGTTCTGCTCGGCTCGCGCTTGGGCT 764
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                                                                                                                                                               .....AlaTyr 140
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/lab_host="DH10B-R"
/note="vector: pOTB7"
a 727 c 679 g 574 t
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0.882
42.593
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Gaps: 21
Percent Identity: 23.045
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	: gb_htc:BC020267	seq_name
	CAGATC 1555	1550
	AlaLeu 365	364
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347 1499	AspProValProSerMetSerPheGlyAlaGlyMetArgT	334 1450
333 1449	ArgTyrAspArgProAspAspPheAspIleGluArg	322 1400
321 1399	rgAspAspValValValValLeuAlaGlyAlaAlaAsnArgAspProArg	305 1350
305 1349	nThrArgGlnLeuAspValAspValGluLeuArgGlyArgArgLeuArgA :::	288 1300
288 1299	AlaGlnAlaValGluGluCysLeuArgTyrAspProSerValGlnSerAs ::: ::: ::: AAGGCGGTGGTCAAGGAAGTGCTAAGACTGCTACCCTGTGGTACCTGGAAA	272 1250
271 1249		260 1203
259 1202	P ; AGTCCAGACAGCACTCCACTCAGAGATCACAGCTGCCCTGAGCCCTGGCT	259 1153
259 1152	ValalaSerGlnValGlyAsnAlaValLeuSerLeuLeuAlaHisProAs ::::: ::::: ::: :: :: 	243 1103
242 1102	IleValSerThrValValThrPheIlePheThrGlyHisGluThr :::::::: :::::::::: AGTCCATCCTGGGAAATGTGACAGAGTTGCTATTGGCGGGAGTGGACACG	228 1053
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21 4 1002	ArgArgGluGlyGlyGluAspLeuLeuAlaLeuMe	203 953
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805		765

seq_documentation_block:
LOCUS BC020267

Homo sapiens, clone IMAGE:4580963, BC020267

mRNA mRNA.

linear

HTC 19-DEC-2001

DEFINITION ACCESSION

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REFERENCE
AUTHORS
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KEYWORDS
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US-09-724-797-36 x BC020267
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: BC020267
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JOURNAL
  266
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                                                                                                        216 CAAGGGGGGCTGTCGAGGCTACACGAGCTGCAGGTGCAGGGCGCCGCGC
                                                                                                                                                                                                              166 GCAGACATCCCAGGCCCCTCTACGCCCAGCTTTCTGGCCGAACTTTTCTG 215
                                34 isArgGlyAlaHisArgValTrpTyrValSerArgPheAlaAspValArg 50
                                                                                                                                                            25
                                                                                                                                                                                                                                                            14 AlaAspValArgArgAspProTyrProSerTyr.......
ACTTCGGGCCG.....GTGTGGCTAGCCAGC...TTTGGGACAGTGCGC 306
                                                                                                                                                       USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
Tissue Procurement: ATCC
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 13904864
This clone has the following problem: no cloning site /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (19-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
DNA Sequency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microdeletion
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1 (bases 1 to 2492)
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Eukaryota; M
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0.882
42.593
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Gaps: 21
Percent Identity: 23.045
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259	7	3 7 0
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21 4 1002	G A	203 953
202 952	Glu.PheAlaAspTyrValGluArgAlaLeuAlaArgArg ::: ::::::: ::: ACTGGGACCAGATGTTTGCATTTGCTCAGAGGCACGTGGAGCGGCGA	190 906
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170 805	uProAlaAlaAspTrpGlyAlaValGlyArgTrpSerArgAspValGlyA :: :: :: :: ::	153 765
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714	GCAGGCGTCGGGGGCGCCCTACCAGAGCCTCCCC	665
140	AlaTyr	139
138 664	laspGluLeu	135 615
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124 573	GTCTGAGG	114 524
114 523	lValGlyProAlaPheSerProSerAlaLeuArgArgLeuGluProV:::::: :: ::: : : : : :	98 474
98 473	ASPIleIleLeuPheGlnASpGluProASpH1SGlyArgLeuArgGlyVa ::: ::: :::: CTGCTCACTGCGGAAGGCGAAGAATGGCAAAGGCTCCGCAGTCT	82 430
429	 TGCCGCCAGCGGGCTTGCGGA	407
81	lγ	70
69 406	rGlylleArgArgPheTrpThrAsp	61 357
61 356	AlaValLeuGlyAspGluArgPheAlaArgTh ::: ::: aCCGTGTACGTGGCCCCTGCACTCGTCGAGGAGCTGCTGCTGCACAGGA	51 307

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1203 CCAGTGCCTACCCCTCAGCCACTGTTCTGTCCCAGCTGCCC...CTGCTG 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347 yrCysLeuGlySerTyrLeuAlaArgThrGlnLeuArgAlaAlaValAla 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 nThrArgGlnLeuAspValAspValGluLeuArgGlyArgArgLeuArgA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTCCAGACAGCACTCCACTCAGAGATCACAGCTGCCCTGAGCCCTGGCT 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cretaregegagacgccregcagagcgregaaregcaaaregcrrragcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCTCGTGTCCCAGACAAAGACATTCATGTGGGTGACTATATTATCCCCA
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                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lhnl.gov
Plate: LLAM11305 row: n column: 13
High quality sequence stop: 717.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 717)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp mRNs musculus
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          Site_1: NotI;
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US-09-724-797-36 x BI246899
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                                                                                                   SOURCE
                                                                                                                                                                          ACCESSION
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                                                                                                                                                                                                                                                                                          seq_name: gb_est2:BG204536
            REFERENCE
                                                                                                                            KEYWORDS
                                                                                                                                                   VERSION
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                                                                              ORGANISM
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                                                                                                                                                                                                                                                                                                                                                TGGGAATGGACCCAGGAACTGCCTTGGCATGAGGTTG
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                                                                                                                                                 RST23942 Athersys RAGE Library Homo
BG204536
BG204536.1 GI:13726223
       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 789)
                                                                              Homo sapiens
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56.983
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s cDNA, mRNA sequence
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REFERENCE AUTHORS

TITLE

JOURNAL COMMENT

FEATURES

source

/organism="Mus musculus"

VERSION KEYWORDS

BI246899.1 GI:14791308

ACCESSION DEFINITION

BI246899 mRNA sequence.

SOURCE

ORGANISM

Mus musculus

house mouse.

seq_documentation_block: LOCUS BI246899

717 602959455F1 NCI_CGAP_Li9 Mus

seq_name: gb_est2:BI246899

1550 CAGATC 1555

364 AlaLeu

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COMMENT
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US-09-724-797-36 x BG204536
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ORIGIN
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410 GAATGAAACGCTCAGATTATTCCCAATTGCTATGAGACTTGAGAGGGTCT 459
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                                                                                                    360 CCACCCACCTATGATACTGTGCTACAGATGGAGTATCTTGACATGGTGGT
                                                                                                                                                                                                                                                    260 lnLeuAspLeuLeuArgArgArgProAsp......
                                                                                                                                                                                                                                                                                                               GAGCAGTGTTCTCCTTCATTATGTATGAACTGGCCACTCACCCTGATG 309
                                                                                                                                                                                                                                                                                                                                                                                                                 GAGCTCGTGGCCCAATCAATTATCTTTATTTTTTGCTGGCTATGAAACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluIleValSerThrValValThrPheIlePheThrGlyHisGluThrVa 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTCTCAGAATTCAAAAGAAACTGAGTCCCACAAAGCTTTGTCCGATCTG
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                                              lGluGluCysLeuArgTyrAspProSerValGlnSerAsnThrArgGlnL 292
                                                                                                                                                                                                        TCCAGCAGAAACTGCAGGAGGAAATTGATGCAGTTTTACCCAATAAGGCA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Kiika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, E., Veloso, N., Kiika, A., Hess, J., Cothren, K., Lo, K., Offenbacher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3201 Carnegie Ave, Cleveland, OH 44115,
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Creation of genome-wide protein expression activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E., Veloso,N., Klika,A., H., J., Danzig,J. and Ducar,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
//db_xref="taxon:9606"
//clone_llb="Athersys RAGE Library"
//cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
/note="See 'Creation of Genome-wide Protein Expression',
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

44 a 176 c 160 g 209 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rry sequence stop: Location/Qualifiers
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LOCUS BG206682
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BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
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MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             510 GTGATGATTCCAAGCTATGCTCTTCACCGTGACCCAAAGTACTGGACAGA 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309 ValValLeuAlaGlyAlaAlaAsnArgAspProArgArgTyrAspAr 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        660 GCCATGAGGTTTGCTCTCATGAACATGAAA......CTTGCTCTAAT 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 GlySerTyrLeuAlaArgThrGlnLeuArgAlaAlaValAlaAlaLeuAl 366
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Creation of genome-wide protein expression libraries using random activation of gene expression
activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3201 Carnegie Ave, Cleveland,
                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 755)
                       231
                                                                                                                                                                                                                                                                                                                                                                                 scain@athersys.com
                  Libraries using Random Activation of Gene Expression, Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                                                                                                                                                                          /clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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alignment_scores:

Quality: Ratio:

179.00 1.584

Length: Gaps:

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REFERENCE
AUTHORS
                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                     seq_documentation_block:
LOCUS BG182832
                                                                                                                                                  DEFINITION
ACCESSION
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                                                                                               SOURCE
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                                                                          ORGANISM
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 765)
                                                                                                                                                           RST1693 Athersys RAGE Library
   Harrington, J.J.,
                                                                                                              BG182832.1 GI:13704503
EST.
                                                                          Homo sapiens
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Sherf, B., Rundlett, S.,
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Jackson, P.D., Perry, R.,
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GAATGAAACGCTCAGATTATTCCCAATTGCTATGAGACTTGAGAGGGTCT 459
                                                                                                                                                                                                                                     lnLeuAspLeuLeuArgArgArgProAsp.......
                                                                                                                                                                                                                                                                                             GAGCAGTGTTCTCCTTCATTATGTATGAACTGGCCACTCACCCTGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GluIleValSerThrValValThrPheIlePheThrGlyHisGluThrVa 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTCTCAGAATTCAAAAGAAACTGAGTCCCACAAAGCTCTGTCCGATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spAlaHisAsp......ArgGlyLeuMetSerArgAsn
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                                                                                             CCACCCACCTATGATACTGTGCTACAGATGGAGTATCTTGACATGGTGGT 409
                                                                                                                                          .....LeuLeuAlaGlnAlaVa 275
                                                                                                                                                                                          TCCAGCAGAAACTGCAGGAGGAAATTGATGCAGTTTTACCCAATAAGGCA
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Creation of genome-wide protein expression libraries using random activation of gene expression
activation of gene expression
activation of gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: Location/Qualifiers
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Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Scott J. Cain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3201 Carnegie Ave, Cleveland, OH 44115, USA
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1.584
53.052
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/dbxrefs-taxon:9606"
/coln_libe="Athersys RAGE Library"
/coll_line="HT1080"
/coll_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression'
/note="See 'Creation of Genome-wide Protein Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
a 172 c 154 g 202 t
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325

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seq_name: gb_est1:AI323114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCTGAGAAGTTCCTCCCTGAAAGATTCAGCAAGAAGAACAAGGACAACA 609
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AI323114 gí:4057543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
Washington University School of Medic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dut
Geisel, S., Kucaba, T., Lacy, M., De, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This read is a RESEQUENCE of a previously sequenced mouse This read has been verified (found to hit its original sel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 814)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       correct orientation)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
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Location/Qualifiers
                            (Pharmacia). Library went through one round
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/clone="IMAGE:483053"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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LOCUS BG195942
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BG195942
        BG195942.1 GI:13717517
EST.
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COMMENT

FEATURES

Homo

nRNA linear EST 21-APR-2001 sapiens cDNA, mRNA sequence.

ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE

AUTHORS

DEFINITION

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normalization to a Cot = 5. Library constructed by Be
Soares and M.Fatima Bonaldo. RNA was kindly provided
Dr. Minoru Ko (Wayne State University)."
167 c 182 g 211 t 2 others
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Align seg 1/1 to: AI323114
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                                                                                                                                  yAlaGlyMetArgTyrCysLeuGlySerTyrLeuAlaArgThrGlnLeuA 359
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                                                                                          GAGTGGACCAAGGAACTGCATTGGCATGAGGTTTGCTCTCATAAACATGA 587
                                                                                                                                                                                                                                                                                                                                                                                  ATTCATTCCCAAAGGGACTGTGGTGATGATACCAACCTTTGCTCTTCACA 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGGAAGACTTGAGAGGGTCTGTAAGACAGATGTTGAAATCAATGGGCT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValGlnSerAsnThrArgGlnLeuAspValAspValGluLeuArgGlyAr 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGCTGGCCATTCACCCTGATGTACAGAAGAAACTTCAGGATGAAATTGA 237
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AAGTTGCTCTT
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                                                                                                                                                                                       lAlaSerGlnValGlyAsnAlaValLeuSerLeuLeuAlaHisProAspG
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                                                                                        lnLeuAspLeuLeuArgArgArgProAsp.....
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Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athers;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nat. Bio
21227151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzid, J., and Ducar, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Creation of genome-wide protein expression libraries using random activation of gene expression Nat. Bitechnol. 19 (5), 440-445 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 828)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Scott J. Cain
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1.379
51.613
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/cell_line="HT1080"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 646 TAGATCCTTACATATACACACCCTTTGGAAGTGGACCCAGAAACTGCATG
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3 (sites)
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Konno,H., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwake,S., Inoue,K., Togawa,Y., Izawa,N., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                               Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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High-efficiency full-length cDNA cloning
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Physical and Chemical Research (RIKEN), Camomic Sciences Center (GSC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XhoI. Host: SOLR.
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5 (bases 1 to 2930)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Please visit our web site (http://genome.gsc.riken.go.jp/) for
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/db_xref="GI:12836111"
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NFLDVNNEQANILVNKLEKHVNQEAFNCFFYITLCALDIICETAMGKNIGAQSNNDSE
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                                                                                                                                                                                                                                 kallikrein B,
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/db_xref="MGD:MGI:1907223"
YVRTVYRMSDMIYRRMKMPWLWFDLWYLVFKEGRDHKRGLKCLHTFTNNVIAERVKER
                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                       /note="data source:MGD,
                                                                                                                                                                                                                                                                                                                     /gene="Klkb1"
                                                                                                                                                                                                                                                                                                                                                                   /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="lung"
/clone_lib="RIKEN fo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="1200012E24"
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/strain="C57BL/6J"
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                                                                   1522 ATCCAGAGGAATTCCGACCAGAGCGGTTCTTTCCTGAAAATTCCCAAGGA 1571
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AAAINMSLYLLGTNPEVQRKVDGELDEVFGRSHRPVILEDLKKLKYLDCVIKETLRVF
PSVPLEARSLEEDCEVGGYKYTKGTEAAIIPXALHRDDRYFPDPEETRREFFPENG
GRHPYAYVPFSAGPRNCIGQKFAVMEEKTILACILRQFWVESNOKREELGLAGDLILR
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Ratio:
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1 (bases 1 to 817)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,N., Hess,J., Cothren,K., Lo,K., Offenbacher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,E., Veloso,N., Klika,A., Hess,J., Cotnren,K., LU,R., CITERLAURE, J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: scain@athersys.com
High quality sequence stop: 495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Scott J. Cain
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                                                                                                                                                                                                                                                                                                                                                                                                                           /Organism="Homo sapiens"
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/clone_lib="Athersys RAGE Library"
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/note="See 'Creation of Genome-wide Protein Expression / note="see 'Creation of Genome-wide Protein Expression',
Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
                                                                                                                                                                                                                                                                                  175.00
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SOURCE
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LOCUS BG208878
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                                                                                                                            Athersys, Inc.
3201 Carnegie Ave, (
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                        Nat. Biotechnol. 19 (5), 440-
                                                                                                                                                                                                                                                                                                 ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random
                                                                                                                                                                                                                                                                                                                                                  Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith
                                                                                                                                                                                                               Contact: Scott J. Cain
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                               1: scain@athersys.com quality sequence stop: 512.
                                             1. .808
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/db_xref="taxon:9606"
                                                            Location/Qualifiers
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660 GGCATGAGGTTTGCTCTCATGAACATGAAACTTGCTCTA
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                                               GlySerTyrLeuAlaArgThrGlnLeuArgAlaAlaVal 362
                                                                                               TAGATCCTTACATATACACACCCTTTGGAAGTGGACCCAGAAACTGCATT
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/note="See 'Creation of Genome-wide Protein Expression
/ibraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

a 180 c 159 g 220 t 3 others
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227 160

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360 270

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lAlaSerGlnValGlyAsnAlaValLeuSerLeuLeuAlaHisProAspG
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                                                                                  GluIleValSerThrValValThrPheIlePheThrGlyHisGluThrVa
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RST16556 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
BG197314
BG197314.1 GI:13719001
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Tel: 216 431 9900
Fax: 216 361 9596
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Athersys, Inc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

a 177 c 168 g 209 t
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1.518
53.521
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2	61	261 GAGCAGTGTTCTCTCATTATGTATGAACTGGCCACTCACCCTGATG 310	10
Ν	260	lnLeuAspLeuLeuArgArgArgProAsp	269
w	311	TCCAGCAGAAACTGCAGGAAGAATTGATGCAGTTTTACCCAATAAGGCA	360
N	270	LeuLeuAlaGlnAlaVa	275
(LI)	361	CCACCCACCTATGATACTGTGCTACAGATGGAGTATCTTGACATGGTGGT	410
N	275		292
4	411	GAATGAAACGCTCAGATTATTCCCAATTGCTATGAGACTTGAGAGGGTCT 4	460
N	292	euAspValAspValGluLeuArgGlyArgArgLeuArgArgAspAspVal	308
4	461	GCAAAAAAGATGTTGAGATCAATGGGATGTTCATTCCCAAAGGGGTGGTG	510
(4)	309	ValValValLeuAlaGlyAlaAlaAsnArgAspProArgArgTyrAspAr	325
(1)	511	GGGATGATTCCAAGCTATGCTCTTCACCGTGACCCAAAGTACTGGACAGA	560
60	325	gProAspAspPheAspIleGluArg	333
t m	561	GCCTGAGAAGTTCCTCCCTGAAAGATTCAGCAAGAAGAACAAGGACAACA	610
1.1	334		349
a	611	TAGATCCTTACATATACACACCCTTTGGAAGTGGACCCAGAAACTGCATT	660
[4]	350	GlySerTyrLeuAlaArgThrGlnLeuArgAlaAlaVal 362	
_	2	661 GGCATGAGGTTTGGTCTCATGAACATGAAACTTTGCTTA 699	

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